WEST Search History

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DATE: Tuesday, April 13, 2004

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND	
☐	L1	ure near10 i	129479
☐	L2	L1 and helicobacter	7
☐	L3	urei.clm. or ure-i.clm.	36
☐	L4	L3 not l2	34
☐	L5	aime	4109
☐	L6	L5 and helicobacter	2
☐	L7	('6248551' |'20030180330')!.PN.	4
☐	L8	aliphatic near5 amidase	34
☐	L9	L8 and (pylori or helicobacter or pyloris or pylroi or pyloridis or pylorum or hpylori or h-pylori)	9

END OF SEARCH HISTORY

WEST Search History

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DATE: Tuesday, April 13, 2004

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=AND		
☐	L1	ure near10 i	129479
☐	L2	L1 and helicobacter	7
☐	L3	urei.clm. or ure-i.clm.	36
☐	L4	L3 not l2	34
☐	L5	aime	4109
☐	L6	L5 and helicobacter	2
☐	L7	('6248551'|'20030180330')!.PN.	4

END OF SEARCH HISTORY

First Hit

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L9: Entry 1 of 9 File: PGPB Feb 19, 2004

DOCUMENT-IDENTIFIER: US 20040033549 A1
TITLE: Quorum sensing signaling in bacteria

Detail Description Paragraph:
[0088] The term "biofilm-associated disease or disorder" includes diseases, disorders or conditions which are characterized or caused by the presence or potential presence of a biofilm, e.g., a bacterial biofilm. Biofilm-associated diseases or disorders include infection of the subject by one or more bacteria, e.g., Pseudomonas aeruginosa, Bacillus subtilis, Candida albicans, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Helicobacter pylori, Escherichia coli, Salmonella typhimurium, Legionella pneumophila, or other gram-negative or gram positive bacteria. Examples of biofilm-associated diseases or disorders include diseases or disorders caused by, for example, bacteria (e.g., gram-positive and/or gram-negative bacteria), fungi, viruses and parasites. Examples of biofilm-associated diseases or disorders include, but are not limited to, cystic fibrosis, AIDS, middle ear infections, osteomyelitis, acne, dental cavities, prostatitis, abscesses, bacteremia, contamination of peritoneal dialysis fluid, endocarditis, pneumonia, meningitis, cellulitis, pharyngitis, otitis media, sinusitis, scarlet fever, arthritis, urinary tract infection, laryngotracheitis, erysipeloid, gas gangrene, tetanus, typhoid fever, acute gastroenteritis, bronchitis, epiglottitis, plague, sepsis, chancroid, wound and bum infection, cholera, glanders, periodontitis, genital infections, empyema, granuloma inguinale, Legionnaire's disease, paratyphoid, bacillary dysentary, brucellosis, diphtheria, pertussis, botulism, toxic shock syndrome, mastitis, rheumatic fever, eye infections, including contact lens infections, periodontal infections, catheter- or medical device-associated infections, and plaque. Other biofilm-associated diseases or disorders include swine erysipelas, peritonitis, abortion, encephalitis, anthrax, nocardiosis, pericarditis, mycetoma, peptic ulcer, melioidosis, Haverhill fever, tularemia, Moko disease, galls (such as crown, cane and leaf), hairy root, bacterial rot, bacterial blight, bacterial brown spot, bacterial wilt, bacterial fin rot, dropsy, columnaris disease, pasteurellosis, furunculosis, enteric redmouth disease, vibriosis of fish, and fouling of medical devices.

Detail Description Table CWU:
6TABLE 6 Quorum-repressed genes..sup.1 Maximum repression (fold).sup.c lasI.sup.- rhlI.sup.- mutant Wt vs. Gene no..sup.a Description.sup.b 3OC12-HSL C4 + 3OC12-HSL lasR.sup.- rhlR.sup.- PA0165 hypothetical protein -2.7 -2.9 (2.0) -4.8 (2.0) PA0433 hypothetical protein -6.8 -19.7 (2.0) -8.9 (1.4) PA0434 hypothetical protein -7.7 -8.5 (2.0) -5.6 (2.0) PA0435 hypothetical protein -9.4 -25.5 (2.0) -33.8 (2.0) PA0485 conserved hypothetical protein.sup.c -1.7 -3.4 (1.4) -3.0 (3.0) PA0887 acsA, acetyl-coenzyme A synthetase -3.3 -4.2 (2.0) -3.6 (3.0) PA1559 hypothetical protein -2.4 -3.5 (2.0) -3.2 (1.4) PA2007 maiA, maleylacetoacetate isomerase -3.2 -1.4 (4.0) -3.2 (3.0) PA2008 fahA, fumarylacetoacetase -3.7 -1.5 (4.0) -2.6 (3.0) PA2009 hmgA, homogentisate 1,2-dioxygenase -4.0 -1.5 (4.0) -2.7 (3.0) PA2250 lpdV, lipoamide dehydrogenase-Val -3.1 -1.8 (4.0) -2.6 (3.0) PA2338 probable component of ABC maltose transporter -5.0 -3.2 (3.0) -4.2 (3.0) PA2339 probable maltose/mannitol transport protein - 1.9 -6.8 (3.0) -4.1 (3.0) PA2340 probable maltose/mannitol transport protein - 3.4 -2.0 (3.0) -3.7 (3.0) PA2341 probable component of ABC maltose transporter -3.1 -2.0 (3.0) -4.2 (3.0) PA2343 mtlY, xylulose kinase -1.7 -

4.0 (3.0) -3.2 (4.0) PA3038 probable porin -2.3 -3.5 (2.0) -4.4 (3.0) PA3174 probable transcriptional regulator -2.1 -3.5 (4.0) -6.5 (3.0) PA3205 hypothetical protein -1.3 -3.1 (4.0) -3.1 (4.0) PA3233 hypothetical protein -2.2 -2.7 (3.0) -5.1 (3.0) PA3234 probable sodium: solute symporter -4.5 -3.4 (2.0) -7.0 (3.0) PA3235 conserved hypothetical protein -3.9 -4.2 (3.0) -6.6 (3.0) PA3281 hypothetical protein -5.7 -6.4 (1.4) -24.9 (1.4) PA3282 hypothetical protein -8.5 -8.8 (1.4) -21.3 (1.4) PA3283 conserved hypothetical protein -9.0 -8.8 (1.4) -27.7 (1.4) PA3284 hypothetical protein -7.1 -10.4 (2.0) -24.3 (1.4) PA3364 amiC, aliphatic amidase expression-regulating protein -2.7 -1.8 (4.0) -2.7 (1.4) PA3365 probable chaperone -3.0 -1.7 (4.0) -4.0 (1.4) PA3575 hypothetical protein -1.6 -2.7 (1.4) -3.3 (2.0) PA3790 oprC, outer membrane protein OprC -2.7 -3.7 (2.0) -4.6 (2.0) PA4359 conserved hypothetical protein -1.4 -2.7 (2.0) -2.8 (1.4) PA4371 hypothetical protein -1.9 -4.1 (2.0) -2.8 (1.4) PA4442 cysN, ATP sulfurylase GTP-binding subunit -2.8 -3.4 (3.0) -7.6 (2.0) PA4443 cysD, ATP sulfurylase small subunit -3.1 -3.4 (3.0) -6.5 (2.0) PA4691 hypothetical protein -2.5 -2.8 (2.0) -2.9 (2.0) PA4692 conserved hypothetical protein -3.8 -3.4 (2.0) -5.0 (1.4) PA4770 lldP, L-lactate permease -1.8 -3.7 (2.0) -5.0 (2.0) PA5168 probable dicarboxylate transporter -2.7 -1.9 (4.0) -5.8 (2.0) .sup.aGene Identification Number from the Pseudomonas genome project (www.pseudomonas.com). .sup.bMaximum changes in gene expression (rounded to two significant figures) in the signal generation mutant in the presence of the signal(s) indicated compared with the absence of signal and in wild-type P. aeruginosa strain compared with the receptor mutant. The values in the parentheses are the OD.sub.600 at which the earliest change of .gtoreq.2.5 was observed (for the signal generation mutant, both time courses were considered). NC, no change. .sup.cThere is a las-rhl box-like sequence with an HI of .gtoreq.10 and <13.

First Hit Fwd Refs

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L9: Entry 6 of 9 File: USPT Feb 20, 2001

US-PAT-NO: 6190667
DOCUMENT-IDENTIFIER: US 6190667 B1

TITLE: Methods of inhibiting Helicobacter pylori

DATE-ISSUED: February 20, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
De Reuse; Hilde	Paris			FR
Skouloubris; Stephane	Paris			FR
Cussac; Valerie	Paris			FR
Labigne; Agnes	Burress/Yvette			FR

US-CL-CURRENT: 424/234.1; 424/780, 435/32

CLAIMS:

We claim:

1. A method for screening a molecule capable of inhibiting the growth or survival of Helicobacter, comprising:

(a) contacting a parental Helicobacter strain with said molecule in a biological sample and contacting a Helicobacter strain deficient in UreI with said molecule;

(b) comparing the acidity sensitivity of the parental strain to the acidity sensitivity of the UreI deficient strain, both of which have been contacted with the molecule of step (a); and

(c) selecting said molecule that increases the acidity sensitivity of the parental strain as compared to the effect of said molecule on the acidity sensitivity of the UreI deficient strain, wherein acidity sensitivity is correlated with inhibiting Helicobacter growth or survival.

2. The method according to claim 1, wherein the acidity sensitivity is evaluated by measuring acidity resistance of the strains.

3. The method according to claim 1, wherein the molecule inhibits UreI activity.

4. The method according to claim 1, wherein the Helicobacter strain is selected from the group consisting of Helicobacter pylori, Helicobacter felis, Helicobacter helmannii, Helicobacter mustalae, Helicobacter canis, Helicobacter bilis, and Helicobacter hepaticus.

5. The method according to claim 1, wherein the molecule has a high affinity for UreI.

6. The method according to claim 1, wherein the molecule inhibits transport of urea or amide analogs.

7. The method according to claim 4, wherein the Helicobacter strain is Helicobacter pylori.

8. The method according to claim 1, wherein said Helicobacter strain deficient in UreI has wild type levels of urease activity.

9. The method according to claim 8, wherein the Helicobacter strain is Helicobacter pylori.

10. The method according to claim 9, wherein in step (b) acidity sensitivity is tested in the presence of urea.

11. The method according to claim 2, wherein acidity resistance is tested in the presence of urea.

L9: Entry 5 of 9 File: USPT Jun 19, 2001

DOCUMENT-IDENTIFIER: US 6248551 B1
TITLE: Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences encoding those polypeptides

Abstract Text (1):
This invention relates to Helicobacter species aliphatic amidase AmiE polypeptides, the DNA encoding those polypeptides and transformed microorganisms capable of expressing those polypeptides. This invention also relates to the use of Helicobacter sp. (particularly Helicobacter pylori) amidase AmiE polypeptides and antibodies specific for those polypeptides in immunogenic, therapeutic, and diagnostic applications. The invention additionally relates to processes of producing Helicobacter species aliphatic amidase AmiE polypeptides and intermediates intermediates useful in the production of those polypeptides.

Brief Summary Text (1):
This invention relates to Helicobacter species aliphatic amidase AmiE polypeptides, the DNA encoding those polypeptides, and transformed microorganisms capable of expressing those polypeptides. In addition, this invention relates to the use of Helicobacter sp. particularly Helicobacter pylori) amidase AmiE polypeptides and antibodies specific for those polypeptides in immunogenic, therapeutic and diagnostic application.

Brief Summary Text (3):
An aliphatic amidase is an acylamide amidohydrolase (E.C. 3.5.1.4) (Merck Index). It It hydrolyses short-chain aliphatic amides (C1-C4 such as acrylamide, acetamide, propionamide or isobutyramide) to produce ammonia and the corresponding organic acid. In addition, an aliphatic amidase possesses acyl transferase activity, i.e., it is able to transfer the acyl group of amides to hydroxylamine to form an acyl hydroxamate plus ammonia.

Brief Summary Text (4):
Aliphatic amidases have been identified in Pseudomonas aeruginosa (Brammar et al., 1987) and Rhodococcus sp. R312 (previously named Brevibacterium sp. R312; Soubrier et al., 1992). Other aliphatic amidases have been identified in Methylophilus methylotrophus (Silman et al., 1991), Arthrobacter sp. J-1 (Asano et al., 1982), and Alcaligenes eutrophus (Friedrich and Mitrenga, 1981). However, no molecular characterization of these latter three enzymes has been reported.

Brief Summary Text (5):
Aliphatic amidases are cytoplasmic enzymes; they have very similar enzymatic properties and molecular masses (38.4 kDa for P. aeruginosa; 38.2 kDa for Rhodococcus sp. R312; 37.8 kDa for M. methylotrophus; and 39 kDa for Arthrobacter sp. J-1), and have either a tetra-, hexa-, or octameric structure. Some of these amidases have been shown to be inducible by their amide substrate. Database searches with the amino acid sequences of these aliphatic amidases indicates that they are more closely related to nitrilases (which catalyze the direct cleavage of nitrites to ammonia and to the corresponding acid) than to the nitrile hydratases (which hydrolyze nitrites to produce amides) or amidases from other classes (Novo et al., 1995).

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### Status: Signed Off. (6 minutes)

### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 04.02.00D

Last logoff:  13apr04 11:40:01
Logon file405 13apr04 12:03:16
*
*
* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
* * * INSTALLED   * * *
SYSTEM:HOME
Cost is in DialUnits
Menu System II: D2 version 1.7.9 term=ASCII
                     *** DIALOG HOMEBASE(SM) Main Menu ***

 Information:
  1.  Announcements (new files, reloads, etc.)
  2.  Database, Rates, & Command Descriptions
  3.  Help in Choosing Databases for Your Topic
  4.  Customer Services (telephone assistance, training, seminars, etc.)
  5.  Product Descriptions

 Connections:
  6.  DIALOG(R) Document Delivery
  7.  Data Star(R)

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      /H = Help            /L = Logoff          /NOMENU = Command Mode


Enter an option number to view information or to connect to an online
 service.  Enter a BEGIN command plus a file number to search a database
(e.g., B1 for ERIC).
? b 155 medicine

       13apr04 12:03:21 User228206 Session D2146.1
            $0.00    0.153 DialUnits FileHomeBase
     $0.00  Estimated cost FileHomeBase
     $0.02  TELNET
     $0.02  Estimated cost this search
     $0.02  Estimated total session cost   0.153 DialUnits


SYSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R)  1966-2004/Apr W1
         (c) format only 2004 The Dialog Corp.
*File 155: Medline has been reloaded. Accession numbers
have changed. Please see HELP NEWS 154 for details.
  File   5:Biosis Previews(R)  1969-2004/Apr W1
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  File  34:SciSearch(R) Cited Ref Sci  1990-2004/Apr W1
          (c) 2004 Inst for Sci Info
  File  35:Dissertation Abs Online  1861-2004/Mar
          (c) 2004 ProQuest Info&Learning
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          (c) 2004 BLDSC all rts. reserv.
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          (c) 2004  Elsevier Science B.V.
  File  73:EMBASE  1974-2004/Apr W1
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  File  91:MANTIS(TM)  1880-2003/Aug
          2001 (c) Action Potential
  File  94:JICST-EPlus  1985-2004/Mar W4
          (c)2004 Japan Science and Tech Corp(JST)
  File  98:General Sci Abs/Full-Text  1984-2004/Apr
          (c) 2004 The HW Wilson Co.
  File 135:NewsRx Weekly Reports  1995-2004/Apr W1
          (c) 2004 NewsRx
*File 135: New newsletters are now added. See Help News135 for the
complete list of newsletters.
  File 144:Pascal  1973-2004/Apr W1
          (c) 2004 INIST/CNRS
  File 149:TGG Health&Wellness DB(SM)  1976-2004/Apr W1
          (c) 2004 The Gale Group
  File 156:ToxFile  1965-2004/Apr W2
          (c) format only 2004 The Dialog Corporation
  File 159:Cancerlit  1975-2002/Oct
          (c) format only 2002 Dialog Corporation
*File 159: Cancerlit ceases updating with immediate effect.
Please see HELP NEWS.
  File 162:Global Health  1983-2004/Mar
          (c) 2004 CAB International
  File 164:Allied & Complementary Medicine  1984-2004/Apr
          (c) 2004 BLHCIS
  File 172:EMBASE Alert  2004/Apr W1
          (c) 2004 Elsevier Science B.V.
  File 266:FEDRIP  2004/Feb
         Comp & dist by NTIS, Intl Copyright All Rights Res
  File 369:New Scientist  1994-2004/Apr W1
          (c) 2004 Reed Business Information Ltd.
  File 370:Science  1996-1999/Jul W3
          (c) 1999 AAAS
*File 370: This file is closed (no updates). Use File 47 for more current
information.
  File 399:CA SEARCH(R)  1967-2004/UD=14016
          (c) 2004 American Chemical Society
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Alert feature enhanced for multiple files, etc. See HELP ALERT.
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
          (c) 1998 Inst for Sci Info
  File 444:New England Journal of Med.  1985-2004/Apr W2
          (c) 2004 Mass. Med. Soc.
  File 467:ExtraMED(tm)  2000/Dec
          (c) 2001 Informania Ltd.
*File 467: For information about updating status please see Help News467.

      Set  Items  Description
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?e aliphatic amidase

Ref    Items    RT  Index-term
E1        34       *ALIPHATIC AMIDASE
E2         1        ALIPHATIC AMIDASE AMIE
E3         1        ALIPHATIC AMIDASE OPERON
E4         3        ALIPHATIC AMIDASES
E5         2     1  ALIPHATIC AMIDE
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E6         1        ALIPHATIC AMIDE FEED SUPPLEMENT
E7        47        ALIPHATIC AMIDES
E8         1        ALIPHATIC AMIDES METAL CHELATING AGENTS IRON C
E9         0     1  ALIPHATIC AMIDINE
E10    54717   218  ALIPHATIC AMINE
E11        7        ALIPHATIC AMINE --ADVERSE DRUG REACTION --AE
E12        3        ALIPHATIC AMINE --CLINICAL TRIAL --CT

          Enter P or PAGE for more
?p

Ref    Items   Index-term
E13        1   ALIPHATIC AMINE --DRUG ADMINISTRATION --AD
E14       67   ALIPHATIC AMINE --DRUG ANALYSIS --AN
E15        4   ALIPHATIC AMINE --DRUG COMBINATION --CB
E16       23   ALIPHATIC AMINE --DRUG COMPARISON --CM
E17        1   ALIPHATIC AMINE --DRUG CONCENTRATION --CR
E18       60   ALIPHATIC AMINE --DRUG DEVELOPMENT --DV
E19        5   ALIPHATIC AMINE --DRUG DOSE --DO
E20        2   ALIPHATIC AMINE --DRUG INTERACTION --IT
E21       22   ALIPHATIC AMINE --DRUG THERAPY --DT
E22       44   ALIPHATIC AMINE --DRUG TOXICITY --TO
E23       11   ALIPHATIC AMINE --ENDOGENOUS COMPOUND --EC
E24        1   ALIPHATIC AMINE --INTRADERMAL DRUG ADMINISTRAT

          Enter P or PAGE for more
?s e1-e4
              34  ALIPHATIC AMIDASE
               1  ALIPHATIC AMIDASE AMIE
               1  ALIPHATIC AMIDASE OPERON
               3  ALIPHATIC AMIDASES
      S1      39  E1-E4
?t s1/free/all
>>>"FREE" is not a valid format name in file(s): 399

 1/8/1     (Item 1 from file: 5)
0013460258   BIOSIS NO.: 200200053769
The Helicobacter pylori paralogous amidases: Analysis of their role in vivo
  and distribution of amiE/amiF among Helicobacter species
2001


 1/8/2     (Item 2 from file: 5)
0013332021   BIOSIS NO.: 200100503860
Aliphatic and enantioselective amidases: From hydrolysis to acyl transfer
  activity
2001


 1/8/3     (Item 3 from file: 5)
0013215382   BIOSIS NO.: 200100387221
Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences
  encoding those polypeptides
2001


 1/8/4     (Item 4 from file: 5)
0013183385   BIOSIS NO.: 200100355224
Substitutions of Thr-103-Ile and Trp-138-Gly in amidase from Pseudomonas
  aeruginosa are responsible for altered kinetic properties and enzyme
  instability
2001


 1/8/5     (Item 5 from file: 5)
0013105593   BIOSIS NO.: 200100277432
The AmiE aliphatic amidase and AmiF formamidase of Helicobacter pylori:
  Natural evolution of two enzyme paralogues
2001
```

1/8/6 (Item 6 from file: 5)
0012979581 BIOSIS NO.: 200100151420
Comparative RNA expression profiling analysis of Helicobacter pylori wild-type and cadA ATPase mutants employing whole genome microarrays detects genes physiologically linked to heavy metal resistance in gastric bacteria
2000

1/8/7 (Item 7 from file: 5)
0012651169 BIOSIS NO.: 200000369482
Crystal structure of N-carbamyl-D-amino acid amidohydrolase with a novel catalytic framework common to amidohydrolases
2000

1/8/8 (Item 8 from file: 5)
0012290079 BIOSIS NO.: 200000008392
Crystal structure and induction mechanism of AmiC-AmiR: A ligand-regulated transcription antitermination complex
1999

1/8/9 (Item 9 from file: 5)
0012248978 BIOSIS NO.: 199900508638
Amino acid homologies between human biotinidase and bacterial aliphatic amidases: Putative identification of the active site of biotinidase
1999

1/8/10 (Item 10 from file: 5)
0011231256 BIOSIS NO.: 199800025503
The aliphatic amidase: Another way to produce ammonia in H. pylori?
1997

1/8/11 (Item 11 from file: 5)
0011157503 BIOSIS NO.: 199799791563
Identification and characterization of an aliphatic amidase in Helicobacter pylori
1997

1/8/12 (Item 12 from file: 5)
0010836795 BIOSIS NO.: 199799470855
A Pseudomonas putida capable of stereoselective hydrolysis of nitriles
1997

1/8/13 (Item 13 from file: 5)
0010370983 BIOSIS NO.: 199699005043
Characterization of the gene cluster of high-molecular-mass nitrile hydratase (H-NHase) induced by its reaction product in Rhodococcus rhodochrous J1
1996

1/8/14 (Item 14 from file: 5)
0009473435 BIOSIS NO.: 199497494720
A new family carbon-nitrogen hydrolases
1994

1/8/15 (Item 1 from file: 34)

12480083 Genuine Article#: 771BV Number of References: 43

Title: Acid-responsive gene induction of ammonia-producing enzymes in Helicobacter pylori is mediated via a metal-responsive repressor cascade (ABSTRACT AVAILABLE)
Publication date: 20040200
Journal Subject Category: IMMUNOLOGY; INFECTIOUS DISEASES
Identifiers--KeyWord Plus(R): FERRIC UPTAKE REGULATOR; UREASE ACTIVITY; LOW-PH; **ALIPHATIC AMIDASE;** PHASE VARIATION; EXPRESSION; IDENTIFICATION; PROTEIN; NIKR; FUR

1/8/16 (Item 2 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

12266057 Genuine Article#: 747ZE Number of References: 47
Title: Burkholderia genome analysis reveals new enzymes belonging to the nitrilase superfamily - The amidase of Burkholderia cepacia (hospital isolate) (ABSTRACT AVAILABLE)
Publication date: 20031200
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: Burkholderia genome ; amidase ; nitrilase superfamily
Identifiers--KeyWord Plus(R): PSEUDOMONAS-AERUGINOSA AMIDASE; AMINO-ACID AMIDOHYDROLASE; SITE-DIRECTED MUTAGENESIS; WIDE-SPECTRUM AMIDASE; SUBSTRATE-SPECIFICITY; **ALIPHATIC AMIDASE;** CRYSTAL-STRUCTURE; ESCHERICHIA-COLI; SWISS-MODEL; ACTIVE-SITE

1/8/17 (Item 3 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

12230215 Genuine Article#: 744CM Number of References: 25
Title: Measuring enzymatic activity of a recombinant amidase using Fourier transform infrared spectroscopy (ABSTRACT AVAILABLE)
Publication date: 20031115
Journal Subject Category: BIOCHEMICAL RESEARCH METHODS; BIOCHEMISTRY & MOLECULAR BIOLOGY; CHEMISTRY, ANALYTICAL
Descriptors--Author Keywords: recombinant amidase ; Fourier transform-infrared spectroscopy (FT-IR) ; enzymatic activity ; hydrolysis ; acetamide
Identifiers--KeyWord Plus(R): PSEUDOMONAS AERUGINOSA AMIDASE; **ALIPHATIC AMIDASE;** ASSAY; PURIFICATION; ACETAMIDE; UREA

1/8/18 (Item 4 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

11471559 Genuine Article#: 654YF Number of References: 48
Title: Differential regulation of amidase- and formamidase-mediated ammonia production by the Helicobacter pylori fur repressor (ABSTRACT AVAILABLE)
Publication date: 20030314
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Identifiers--KeyWord Plus(R): FERRIC UPTAKE REGULATOR; UREASE ACTIVITY; GASTRIC COLONIZATION; **ALIPHATIC AMIDASE;** MAILLARD REACTION; ACID RESISTANCE; IDENTIFICATION; PROTEIN; TRANSCRIPTION; EXPRESSION

1/8/19 (Item 5 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

10899399 Genuine Article#: 582RR Number of References: 49
Title: Support for a three-dimensional structure predicting a Cys-Glu-Lys catalytic triad for Pseudomonas aeruginosa amidase comes from site-directed mutagenesis and mutations altering substrate specificity (ABSTRACT AVAILABLE)
Publication date: 20020801
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: comparative modelling ; NitFhit ; nitrilase
Identifiers--KeyWord Plus(R): WIDE-SPECTRUM AMIDASE; ACTIVE-SITE;

ALIPHATIC AMIDASE; CRYSTAL-STRUCTURE; SWISS-MODEL; NITRILASE; CLONING; ENZYME; PROTEINS; DOCKING

1/8/20 (Item 6 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

10782796 Genuine Article#: 569YV Number of References: 68
Title: Cloning and heterologous expression of an enantio selective amidase from Rhodococcus erythropolis strain MP50 (ABSTRACT AVAILABLE)
Publication date: 20020700
Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY; MICROBIOLOGY
Identifiers--KeyWord Plus(R): PSEUDOMONAS-CHLORORAPHIS B23; MASS NITRILE HYDRATASE; ENANTIOSELECTIVE HYDROLYSIS; METHYLOPHILUS-METHYLOTROPHUS; NUCLEOTIDE-SEQUENCE; STRUCTURAL EVIDENCE; **ALIPHATIC AMIDASE;** ESCHERICHIA-COLI; NAPROXEN AMIDE; RHODOCHROUS J1

1/8/21 (Item 7 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

10087744 Genuine Article#: 483HR Number of References: 19
Title: A monoclonal antibody specific for Pseudomonas aeruginosa amidase (ABSTRACT AVAILABLE)
Publication date: 20010800
Journal Subject Category: BIOCHEMICAL RESEARCH METHODS; BIOTECHNOLOGY & APPLIED MICROBIOLOGY; IMMUNOLOGY
Identifiers--KeyWord Plus(R): WIDE-SPECTRUM AMIDASE; DIRECTED EVOLUTION; **ALIPHATIC AMIDASE;** ACTIVE-SITE; PURIFICATION; SEQUENCE; CLONING; FAMILY; ENZYME

1/8/22 (Item 8 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

09783237 Genuine Article#: 448XY Number of References: 42
Title: Molecular and biochemical characterization of the recombinant amidase from hyperthermophilic archaeon Sulfolobus solfataricus (ABSTRACT AVAILABLE)
Publication date: 20010600
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY; MICROBIOLOGY
Descriptors--Author Keywords: Sulfolobus solfataricus ; Archaea ; amidase ; signatured amidase ; thermophiles
Identifiers--KeyWord Plus(R): ENANTIOMER-SELECTIVE AMIDASE; COMPLETE GENOME SEQUENCE; ACYL TRANSFER ACTIVITY; AMINO-ACID SEQUENCE; NITRILE HYDRATASE; PSEUDOMONAS-AERUGINOSA; STRUCTURAL EVIDENCE; **ALIPHATIC AMIDASE;** ESCHERICHIA-COLI; PURIFICATION

1/8/23 (Item 9 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

09030994 Genuine Article#: 358VM Number of References: 32
Title: Steric hindrance regulation of the Pseudomonas aeruginosa amidase operon (ABSTRACT AVAILABLE)
Publication date: 20000929
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Identifiers--KeyWord Plus(R): BINDING ATTENUATION PROTEIN; NIFL-NIFA COMPLEX; TRANSCRIPTION ANTITERMINATION; **ALIPHATIC AMIDASE;** NUCLEOTIDE-SEQUENCE; NITROGEN-FIXATION; CRYSTAL-STRUCTURE; GENE AMIR; RNA; EXPRESSION

1/8/24 (Item 10 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

08553508 Genuine Article#: 299TF Number of References: 32
Title: Amino acid homologies between human biotinidase and bacterial

aliphatic amidases: Putative identification of the active site of biotinidase (ABSTRACT AVAILABLE)
Publication date: 20000200
Journal Subject Category: GENETICS & HEREDITY; MEDICINE, RESEARCH & EXPERIMENTAL; BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: biotinidase ; **aliphatic amidase ;** nitrilase ; active site
Identifiers--KeyWord Plus(R): HUMAN-SERUM BIOTINIDASE; PSEUDOMONAS-AERUGINOSA; COMMON-CAUSE; DEFICIENCY; GENE; NITRILASE; CLONING; BIOSYNTHESIS; PURIFICATION; SEQUENCE

1/8/25 (Item 11 from file: 34)
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08534599 Genuine Article#: 297HP Number of References: 21
Title: Structural adaptation to selective pressure for altered ligand specificity in the Pseudomonas aeruginosa amide receptor, AmiC (ABSTRACT AVAILABLE)
Publication date: 20000200
Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY; BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: crystallography ; ligand specificity ; mutation ; protein evolution ; small molecule binding protein
Identifiers--KeyWord Plus(R): TRANSCRIPTION ANTITERMINATION; **ALIPHATIC AMIDASE;** BINDING-PROTEIN; CRYSTALLIZATION; OPERON; EXPRESSION; ERRORS; GENES; MAPS

1/8/26 (Item 12 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

07798176 Genuine Article#: 209UB Number of References: 23
Title: Evidence that cysteine-166 is the active-site nucleophile of Pseudomonas aeruginosa amidase: crystallization and preliminary X-ray diffraction analysis of the enzyme (ABSTRACT AVAILABLE)
Publication date: 19990615
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Identifiers--KeyWord Plus(R): **ALIPHATIC AMIDASE;** IDENTIFICATION; PURIFICATION; NITRILASE; SEQUENCE; FAMILY; GENE

1/8/27 (Item 13 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

05333966 Genuine Article#: VR218 Number of References: 25
Title: TRANSCRIPTION ANTITERMINATION REGULATION OF THE PSEUDOMONAS-AERUGINOSA AMIDASE OPERON (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY; CELL BIOLOGY
Descriptors--Author Keywords: AMIDASE ; ANTITERMINATION ; PSEUDOMONAS-AERUGINOSA
Identifiers--KeyWords Plus: **ALIPHATIC AMIDASE;** CRYSTAL-STRUCTURE; ESCHERICHIA-COLI; BGL OPERON; GENE AMIR; RNA; EXPRESSION; SEQUENCE; PHOSPHORYLATION; TERMINATION
Research Fronts: 94-3167 002 (RNA FOLDING; SEQUENCE DEPENDENCE OF STABILITY; SECONDARY STRUCTURE MODEL; HIV-1 VIRUS)
94-4806 001 (GENE ORGANIZATION; LONG-CHAIN FATTY-ACID TRANSPORT; TRANSCRIPTION FACTOR)

1/8/28 (Item 14 from file: 34)
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05199091 Genuine Article#: VG565 Number of References: 38
Title: MOLECULAR CHARACTERIZATION OF FORMAMIDASE FROM METHYLOPHILUS-METHYLOTROPHUS (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: FORMAMIDASE ; FMDA ; FMDB ; METHYLOPHILUS METHYLOTROPHUS

Identifiers--KeyWords Plus: ENANTIOMER-SELECTIVE AMIDASE; PROTEIN SECONDARY STRUCTURE; PSEUDOMONAS-AERUGINOSA; NITRILE HYDRATASE; METHANOL DEHYDROGENASE; NUCLEOTIDE-SEQUENCE; CONTINUOUS CULTURE; **ALIPHATIC AMIDASE;** BINDING-PROTEIN; GENE
Research Fronts: 94-4806 001 (GENE ORGANIZATION; LONG-CHAIN FATTY-ACID TRANSPORT; TRANSCRIPTION FACTOR)

1/8/29 (Item 15 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

04402358 Genuine Article#: TA647 Number of References: 26
Title: REGULATION OF NITROGEN-METABOLISM, STARCH UTILIZATION AND THE BETA-HBD-ADHL GENE-CLUSTER IN CLOSTRIDIUM-ACETOBUTYLICUM (Abstract Available)
Journal Subject Category: MICROBIOLOGY
Descriptors--Author Keywords: GENE REGULATION ; CLOSTRIDIUM ACETOBUTYLICUM ; GLUTAMINE SYNTHETASE ; CCPA GENE ; ADHL GENE ; P-HBD GENE
Identifiers--KeyWords Plus: PSEUDOMONAS-AERUGINOSA; BACILLUS-SUBTILIS; NUCLEOTIDE-SEQUENCE; MOLECULAR ANALYSIS; GLUTAMINE-SYNTHETASE; **ALIPHATIC AMIDASE;** EXPRESSION; ANTITERMINATION; ENZYMES; ACETATE

1/8/30 (Item 16 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

04198272 Genuine Article#: RN954 Number of References: 41
Title: IDENTIFICATION OF 2 NEW GENES IN THE PSEUDOMONAS-AERUGINOSA AMIDASE OPERON, ENCODING AN ATPASE (AMIB) AND A PUTATIVE INTEGRAL MEMBRANE-PROTEIN (AMIS) (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Identifiers--KeyWords Plus: ESCHERICHIA-COLI; NUCLEOTIDE-SEQUENCE; **ALIPHATIC AMIDASE;** BINDING PROTEIN; EXPRESSION; CLONING; PURIFICATION; COMPONENTS; PRODUCT; SUBUNIT
Research Fronts: 93-4847 002 (HETEROLOGOUS EXPRESSION; CHROMOSOMAL DNA; GENE ENCODING METHYLMALONYL-COENZYME-A MUTASE)
93-3088 001 (RAT MUSCLE; PROTEIN PHOSPHATASE-1; MAJOR GLUTATHIONE TRANSFERASE)
93-8105 001 (PUTATIVE CATALYTIC ATP-BINDING SITE OF THE BACILLUS-SUBTILIS SECA PROTEIN; CONSERVED MOTIFS; INDEPENDENT DOMAINS)

1/8/31 (Item 17 from file: 34)
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04035936 Genuine Article#: RA622 Number of References: 23
Title: TRANSCRIPTIONAL ANALYSIS OF THE AMIDASE OPERON FROM PSEUDOMONAS-AERUGINOSA (Abstract Available)
Journal Subject Category: MICROBIOLOGY
Identifiers--KeyWords Plus: **ALIPHATIC AMIDASE;** CATABOLITE REPRESSION; NUCLEOTIDE-SEQUENCE; ESCHERICHIA-COLI; AMIE GENE; EXPRESSION; DNA; COMPLEMENTATION; CLONING; PRODUCT
Research Fronts: 93-4847 002 (HETEROLOGOUS EXPRESSION; CHROMOSOMAL DNA; GENE ENCODING METHYLMALONYL-COENZYME-A MUTASE)

1/8/32 (Item 18 from file: 34)
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03080704 Genuine Article#: ND468 Number of References: 22
Title: ARG-188 AND TRP-144 ARE IMPLICATED IN THE BINDING OF UREA AND ACETAMIDE TO THE ACTIVE-SITE OF THE AMIDASE FROM PSEUDOMONAS-AERUGINOSA (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY; BIOPHYSICS
Descriptors--Author Keywords: AMIDASE ; UREA BINDING ; MUTATION ; ACETANILIDASE ; (PSEUDOMONAS-AERUGINOSA)
Identifiers--KeyWords Plus: **ALIPHATIC AMIDASE;** SEQUENCE

1/8/33 (Item 19 from file: 34)
DIALOG(R)File 34:(c) 2004 Inst for Sci Info. All rts. reserv.

02658267 Genuine Article#: LU513 Number of References: 31
Title: ANTITERMINATION OF AMIDASE EXPRESSION IN PSEUDOMONAS-AERUGINOSA IS CONTROLLED BY A NOVEL CYTOPLASMIC AMIDE-BINDING PROTEIN (Abstract Available)
Journal Subject Category: BIOCHEMISTRY & MOLECULAR BIOLOGY
Descriptors--Author Keywords: BINDING PROTEINS ; GENE REGULATION ; SIGNAL TRANSDUCTION
Identifiers--KeyWords Plus: ESCHERICHIA-COLI; NUCLEOTIDE-SEQUENCE; TRANSCRIPTIONAL ANTITERMINATION; SALMONELLA-TYPHIMURIUM; **ALIPHATIC AMIDASE;** BGL OPERON; GENE AMIR; CLONING; TRANSPORT; ALIGNMENT

1/8/34 (Item 20 from file: 34)
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01314772 Genuine Article#: GN696 Number of References: 16
Title: N-TERMINAL AMINO-ACID-SEQUENCE OF BREVIBACTERIUM SP R312 WIDE-SPECTRUM AMIDASE (Abstract Available)
Journal Subject Category: BIOTECHNOLOGY & APPLIED MICROBIOLOGY; MICROBIOLOGY
Identifiers--KeyWords Plus: NITRILE HYDRATASE; PSEUDOMONAS-AERUGINOSA; **ALIPHATIC AMIDASE;** SP STRAIN-R312; PURIFICATION
Research Fronts: 89-3034 001 (MICROTUBULE CROSS-LINKING PROTEIN; SMALL SYNAPTIC VESICLES OF RAT-BRAIN; AXOLININ LOCALIZATION)

1/8/35 (Item 1 from file: 71)
01404571 2000080041
Amino acid homologies between human biotinidase and bacterial aliphatic amidases: Putative identification of the active site of biotinidase

1/8/36 (Item 1 from file: 73)
03918813 EMBASE No: 1989087806
Nucleotide sequence of the aliphatic amidase regulator gene (amiR) of Pseudomonas aeruginosa
1989

1/8/37 (Item 2 from file: 73)
01715617 EMBASE No: 1980083910
Local anesthetics block induction of the Pseudomonas alk regulon
1979

1/8/38 (Item 3 from file: 73)
01507397 EMBASE No: 1979229151
Inhibition of the aliphatic amidase from Pseudomonas aeruginosa by urea and related compounds
1979

1/8/39 (Item 4 from file: 73)
00936651 EMBASE No: 1978064941
Relationship between culture density and catabolite repression of an inducible aliphatic amidase in a thermophilic bacillus
1977
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### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
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DIALOG INFORMATION SERVICES
PLEASE LOGON:
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 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 04.02.00D

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* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
* * * INSTALLED   * * *

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  File  94:JICST-EPlus  1985-2004/Mar W4
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  File  98:General Sci Abs/Full-Text  1984-2004/Apr
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  File 135:NewsRx Weekly Reports  1995-2004/Apr W1
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*File 135: New newsletters are now added. See Help News135 for the
complete list of newsletters.
  File 144:Pascal  1973-2004/Apr W1
         (c) 2004 INIST/CNRS
  File 149:TGG Health&Wellness DB(SM)  1976-2004/Apr W1
         (c) 2004 The Gale Group
  File 156:ToxFile  1965-2004/Apr W2
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  File 159:Cancerlit  1975-2002/Oct
         (c) format only 2002 Dialog Corporation
*File 159: Cancerlit ceases updating with immediate effect.
Please see HELP NEWS.
  File 162:Global Health  1983-2004/Mar
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  File 164:Allied & Complementary Medicine  1984-2004/Apr
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        Comp & dist by NTIS, Intl Copyright All Rights Res
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  File 399:CA SEARCH(R)  1967-2004/UD=14016
         (c) 2004 American Chemical Society
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  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
         (c) 1998 Inst for Sci Info
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         (c) 2004 Mass. Med. Soc.
  File 467:ExtraMED(tm)  2000/Dec
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☐	L6	L4 same (treat$ or prevent$ or therapeut$ or inhibit$ or modulat$ or block$ or inactiv$ or antagon$).clm.	1601
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*File 155: Medline has been reloaded. Accession numbers
have changed. Please see HELP NEWS 154 for details.
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         (c) 2004 Inst for Sci Info
  File 144:Pascal  1973-2004/Apr W1
         (c) 2004 INIST/CNRS
  File 357:Derwent Biotech Res.  _1982-2004/Apr W2
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  File 340:CLAIMS(R)/US Patent  1950-04/Apr 08
         (c) 2004 IFI/CLAIMS(R)
*File 340: Annual reload and classification updates delayed due
 to processing issues.
  File 654:US Pat.Full.  1976-2004/Apr 06
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*File 654: US published applications now online.  See HELP NEWS 654
for details.  Reassignments current through December 2, 2003.
  File 143:Biol. & Agric. Index  1983-2004/Mar
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  File 156:ToxFile  1965-2004/Apr W2
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  File  50:CAB Abstracts  1972-2004/Mar
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        Dist by NAL, Intl Copr. All rights reserved
  File 342:Derwent Patents Citation Indx  1978-04/200420
         (c) 2004 Thomson Derwent
  File 348:EUROPEAN PATENTS  1978-2004/Apr W01
         (c) 2004 European Patent Office
  File 349:PCT FULLTEXT  1979-2002/UB=20040408,UT=20040401
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 2/9/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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13675690   PMID: 9364923
   Identification and characterization of an aliphatic amidase in
Helicobacter pylori.
  Skouloubris S; Labigne A; De Reuse H
  Unite de Pathogenie Bacterienne des Muqueuses, Institut Pasteur, Paris,
France.
  Molecular microbiology (ENGLAND)  Sep 1997, 25 (5) p989-98, ISSN
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0950-382X Journal Code: 8712028
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Record type: Completed
Subfile: INDEX MEDICUS

We report, for the first time, the presence in Helicobacter pylori of an aliphatic amidase that, like urease, contributes to ammonia production. Aliphatic amidases are cytoplasmic acylamide amidohydrolases (EC 3.5.1.4) hydrolysing short-chain aliphatic amides to produce ammonia and the corresponding organic acid. The finding of an aliphatic amidase in H. pylori was unexpected as this enzyme has only previously been described in bacteria of environmental (soil or water) origin. The H. pylori amidase gene amiE (1017 bp) was sequenced, and the deduced amino acid sequence of AmiE (37746Da) is very similar (75% identity) to the other two sequenced aliphatic amidases, one from Pseudomonas aeruginosa and one from Rhodococcus sp. R312. Amidase activity was measured as the release of ammonia by sonicated crude extracts from H. pylori strains and from recombinant Escherichia coli strains overproducing the H. pylori amidase. The substrate specificity was analysed with crude extracts from H. pylori cells grown in vitro; the best substrates were propionamide, acrylamide and acetamide. Polymerase chain reaction (PCR) amplification of an internal amiE sequence was obtained with each of 45 different H. pylori clinical isolates, suggesting that amidase is common to all H. pylori strains. A H. pylori mutant (N6-836) carrying an interrupted amiE gene was constructed by allelic exchange. No amidase activity could be detected in N6-836. In a N6-urease negative mutant, amidase activity was two- to threefold higher than in the parental strain N6. Crude extracts of strain N6 slowly hydrolysed formamide. This activity was affected in neither the amidase negative strain (N6-836) nor a double mutant strain deficient in both amidase and urease activities, suggesting the presence of an independent discrete formamidase in H. pylori. The existence of an aliphatic amidase, a correlation between the urease and amidase activities and the possible presence of a formamidase indicates that H. pylori has a large range of possibilities for intracellular ammonia production.

Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--analysis--AN; *Helicobacter pylori --enzymology--EN; Amino Acid Sequence; Cloning, Molecular; DNA, Recombinant ; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Genes, Structural, Bacterial--genetics--GE; Helicobacter pylori--chemistry--CH; Helicobacter pylori--genetics--GE; Molecular Sequence Data; Mutation --genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins --metabolism--ME; Sequence Homology, Amino Acid; Substrate Specificity
Molecular Sequence Databank No.: GENBANK/Y12252
CAS Registry No.: 0 (DNA, Recombinant); 0 (Recombinant Proteins)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19980129
Record Date Completed: 19980129

2/9/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12684768 PMID: 7607322

Pseudomonas aeruginosa aliphatic amidase **is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.**

Novo C; Tata R; Clemente A; Brown P R
Instituto Nacional de Engenharia e Tecnologia Industrial/IBQTA, Queluz, Portugal.

FEBS letters (NETHERLANDS) Jul 3 1995, 367 (3) p275-9, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

A database search indicated homology between some members of the

nitrilase/cyanide hydratase family, Pseudomonas aeruginosa and Rhodococcus erythropolis amidases and several other proteins, some of unknown function. BLOCK and PROFILE searches confirmed these relationships and showed that four regions of the P. aeruginosa amidase had significant homology with corresponding regions of nitrilases. A phylogenetic tree placed the P. aeruginosa and R. erythropolis amidases in a group with nitrilases but separated other amidases into three groups. The active site cysteine in nitrilases is conserved in the P. aeruginosa amidase indicating that Cys166 is the active site nucleophile.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--chemistry--CH; *Pseudomonas aeruginosa --enzymology--EN; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Binding Sites; Cysteine--chemistry--CH; Hydro-Lyases--chemistry--CH; Molecular Sequence Data; Phylogeny; Sequence Alignment; Sequence Homology, Amino Acid

CAS Registry No.: 52-90-4 (Cysteine)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)

Record Date Created: 19950817

Record Date Completed: 19950817

2/9/7 (Item 7 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

08977358 PMID: 1907262

Cloning and DNA sequence of amiC, a new gene regulating expression of the Pseudomonas aeruginosa aliphatic amidase **, and purification of the amiC product.**

Wilson S; Drew R

Department of Biochemistry, University College London, United Kingdom.

Journal of bacteriology (UNITED STATES) Aug 1991, 173 (16) p4914-21, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Using in vitro-constructed deletions and subcloned DNA fragments, we have identified a new gene, amiC, which regulates expression of the inducible Pseudomonas aeruginosa aliphatic amidase activity. The DNA sequence of the gene has been determined, and an open reading frame encoding a polypeptide of 385 amino acids (molecular mass, 42,834 Da) has been identified. A search of sequence libraries has failed to find homologies with other published sequences. The amiC translation termination codon (A)TGA overlaps the initiation codon for the downstream amiR transcription antitermination factor gene, implying that the amiCR operon is coordinately regulated. Disruption of the amiC open reading frame by insertion and deletion leads to constitutive amidase synthesis, suggesting that AmiC is a negative regulator. This is confirmed by the finding that a broad-host-range expression vector carrying amiC (pSW41) represses amidase expression in a series of previously characterized P. aeruginosa amidase-constitutive mutants. The AmiC polypeptide has been purified from PAC452(pSW41), and N-terminal amino acid sequencing has confirmed the gene identification.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins --isolation and purification--IP; *Genes, Regulator--genetics--GE; *Periplasmic Binding Proteins; *Pseudomonas aeruginosa--genetics--GE; *Repressor Proteins--isolation and purification--IP; Amidohydrolases --biosynthesis--BI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Base Sequence; Enzyme Induction; Escherichia coli--metabolism--ME; Gene Expression Regulation, Bacterial; Molecular Sequence Data; Mutation --genetics--GE; Plasmids--genetics--GE; Pseudomonas aeruginosa--enzymology --EN; Repressor Proteins--genetics--GE; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/M43175; GENBANK/M74478; GENBANK/M74479; GENBANK/M74480; GENBANK/M74481; GENBANK/M74482; GENBANK/M74483; GENBANK/M74484; GENBANK/S45931; GENBANK/S45975;

GENBANK/X13776
CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Plasmids); 0 (Repressor Proteins); 142462-53-1 (AmiC protein, Pseudomonas aeruginosa)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19910905
Record Date Completed: 19910905

2/9/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08102032 PMID: 2495988
Nucleotide sequence of the aliphatic amidase **regulator gene (amiR) of Pseudomonas aeruginosa.**
Lowe N; Rice P M; Drew R E
Department of Biochemistry, University College London, England.
FEBS letters (NETHERLANDS) Mar 27 1989, 246 (1-2) p39-43, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The nucleotide sequence of a 1001 bp ClaI/XhoI DNA fragment encoding the amidase regulator gene (amiR) from Pseudomonas aeruginosa has been determined. The sequence derives from strain PAC433, a constitutive high expressing amidase mutant, and contains two overlapping open reading frames. Analysis of the sequence has identified one of the reading frames as amiR. The gene encodes a 196 amino acid polypeptide which shows a strong bias towards codons with G or C in the third position. The amiR gene shows no sequence homology with other bacterial regulator proteins.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Regulator; *Pseudomonas aeruginosa--genetics--GE; Amino Acid Sequence; Base Sequence; Codon; Deoxyribonucleases, Type II Site-Specific; Molecular Sequence Data; Molecular Weight; Pseudomonas aeruginosa--enzymology--EN; Translation, Genetic
Molecular Sequence Databank No.: GENBANK/X13776
CAS Registry No.: 0 (Codon)
Enzyme No.: EC 3.1.21.- (endodeoxyribonuclease ClaI); EC 3.1.21.- (endodeoxyribonuclease XhoI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific); EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19890608
Record Date Completed: 19890608

2/9/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07448694 PMID: 3108029
The amino acid sequence of the aliphatic amidase **from Pseudomonas aeruginosa.**
Ambler R P; Auffret A D; Clarke P H
FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p285-90, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Amino acid sequence studies show that the aliphatic amidase (EC 3.5.1.4) from Pseudomonas aeruginosa PAC142 consists of a single polypeptide chain of 346 residues, giving an Mr of 38,400. The evidence from the amino acid studies is in complete agreement with that deduced from the DNA sequence of the amiE gene. Studies of the protein from Pseudomonas putida A87 show that it differs from the Ps. aeruginosa protein by about 30 amino acid

substitutions. It now becomes possible to relate changes in the enzyme which result in altered specificity to structural changes in the protein.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--analysis--AN; *Pseudomonas aeruginosa --enzymology--EN; Amino Acid Sequence; Peptide Fragments--analysis--AN
CAS Registry No.: 0 (Peptide Fragments)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19870626
Record Date Completed: 19870626

2/9/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06715270 PMID: 6440948
Complementation analysis of the aliphatic amidase **genes of Pseudomonas aeruginosa.**
Drew R
Journal of general microbiology (ENGLAND) Dec 1984, 130 (Pt 12) p3101-11, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A plasmid, pCL34, capable of autonomous replication in Escherichia coli and Pseudomonas aeruginosa has been constructed which carries the promoter and structural gene (amiE) for P. aeruginosa amidase, but not the regulator gene (amiR). Plasmid pCL34 has been mobilized from E. coli to P. aeruginosa using the broad host range plasmid RP4. Complementation studies were performed in P. aeruginosa strains carrying various amidase mutations. Measurements of amidase activity in the recipients under inducing, non-inducing and repressing conditions showed trans-complementation by the chromosomally located regulator gene product. These results confirmed the positive control model for amidase gene expression. Levels of amidase expression seen during these studies were approximately threefold higher than in the parental, amidase-positive strains.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Chromosome Mapping; Gene Expression Regulation; Genetic Complementation Test; Phenotype; Plasmids; Pseudomonas aeruginosa--enzymology--EN; Transformation, Bacterial
CAS Registry No.: 0 (Plasmids)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19850314
Record Date Completed: 19850314

2/9/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05674138 PMID: 6793036
Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase **from Pseudomonas aeruginosa.**
Hollaway M R; Clarke P H; Ticho T
Biochemical journal (ENGLAND) Dec 1 1980, 191 (3) p811-26, ISSN 0264-6021 Journal Code: 2984726R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
1. Chloroacetone (I) was shown to be an active-site-directed inhibitor of the aliphatic amidase (EC 3.5.1.4) from Pseudomonas aeruginosa strain PAC142.2. This inhibitor reacted with the enzyme in two stages: the first involving the reversible formation of an enzymically inactive species, EI, and the second the formation of a species, EX, from which enzymic activity

could not be recovered. 3. Different types of kinetic experiment were conducted to test conformity of the reaction to the scheme: E + I k+1 Equilibrium k-1 EI Leads to K+2 EX A computer-based analysis of the results was carried out and values of the individual rate constants were determined. 4. No direct evidence for a binding step before the formation of EI could be obtained, as with [E]0 Less Than [I]0 the observed first-order rate constant for the formation of EI was directly proportional to the concentration of chloroacetone up to 1.2 mM (above this concentration the reaction became too rapid to follow even by the stopped-flow method developed to investigate fast inhibition). 5. The value of k+1 exhibited a bell-shaped pH-dependency with a maximum value of about 3 X 10(3) M-1. S-1 at pH6 and apparent pKa values of 7.8 and about 4.8.6. The values of k-1 and K+2 were similar and changed with the time of reaction from values of about 3 X 10(-3) S-1 (pH8.6) at short times to about one-sixth this value for longer periods of incubation. In this respect the simple reaction scheme is insufficient to describe the inhibition process. 7. The overall inhibition reaction is rapid, whether it is considered in relation to the expected chemical reactivity of chloroacetone, the rate of reaction of other enzymes with substrate analogues containing the chloromethyl group, or the rate of the amidase-catalysed hydrolysis of N-methylacetamide, a substrate that is nearly isosteric with chloroacetone. 8. Acetamide protected the amidase from inhibition by chloroacetone, and the concentration-dependence of the protection gave a value of an apparent dissociation constant similar to the Km value for this substrate. 9. Addition of acetamide to solutions of the species EI led to a slow recovery of activity. Recovery of active enzyme was also observed after dilution of a solution of EI in the absence of substrate. 10. The species EI is considered not to be a simple adsorption complex, and the possibilities are discussed that it may be a tetrahedral carbonyl adduct, a Schiff base (azomethine) or a complex in which the enzyme has undergone a structural change. The species EX is probably a derivative in which there is a covalent bond between a group in the enzyme and the C-1 atom of the inhibitor.

Descriptors: *Acetone--analogs and derivatives--AA; *Amidohydrolases --antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetone--pharmacology--PD; Binding Sites; Kinetics; Models, Chemical

CAS Registry No.: 0 (Acetamides); 67-64-1 (Acetone); 78-95-5 (chloroacetone)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19811119

Record Date Completed: 19811119

2/9/13 (Item 13 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05067535 PMID: 110589

Inhibition of the aliphatic amidase **from Pseudomonas aeruginosa by urea and related compounds.**

Gregoriou M; Brown P R

European journal of biochemistry / FEBS (GERMANY, WEST) May 2 1979, 96 (1) p101-8, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The time-dependent inhibition of amidase from Pseudomonas aeruginosa strain AI 3 by urea, hydroxyurea and cyanate displayed saturation kinetics fitting a model for the reaction sequence in which formation of a complex in a reversible step was followed by an irreversible step. Altered amidases from mutant strains AIU 1N and OUCH 4, selected for their resistance to inhibition of growth by urea and hydroxyurea respectively, had altered kinetic constants for inhibition indicating reduced binding capacity for the inhibitors. The substrate acetamide protected AI 3 amidase against inhibition by urea,.and altered Ki values for inhibition of the mutant amidases were paralleled by alterations in Km values for acetamide

indicating that urea acted at the active site. Inhibition of AI 3 amidase involved the binding of one molecule of urea per molecule of enzyme. Urea inhibited amidase slowly regained activity at pH 7.2 through release of urea.

Descriptors: *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; *Urea--pharmacology--PD; Cyanates --pharmacology--PD; Enzyme Activation; Hydroxyurea--pharmacology--PD; Kinetics; Molecular Weight

CAS Registry No.: 0 (Cyanates); 127-07-1 (Hydroxyurea); 57-13-6 (Urea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

2/9/14 (Item 14 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05063754 PMID: 110350

Kinetic mechanism of the aliphatic amidase **from Pseudomonas aeruginosa.**

Woods M J; Findlater J D; Orsi B A

Biochimica et biophysica acta (NETHERLANDS) Mar 16 1979, 567 (1) p225-37, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The kinetic constants for hydrolysis and transfer (with hydroxylamine as the alternate acceptor) of the aliphatic amidase (acylamide amidohydrolase, EC 3.5.1.4) from Pseudomonas aeruginosa were determined for a variety of acetyl and propionyl derivatives. The results obtained were consistent with a ping-pong or substitution mechanism. Product inhibition, which was pH dependent, implicated an acyl-enzyme compound as a compulsory intermediate and indicated that ammonia combined additionally with the free enzyme in a dead-end manner. The uncompetitive activation of acetamide hydrolysis by hydroxylamine and the observation that the partitioning of products between acetic acid and acetohydroxamate was linearly dependent on the hydroxylamine concentration substantiated these conclusions and indicated that deacylation was at least partially rate limiting. With propionamide as the acyl donor apparently anomalous results, which included inequalities in certain kinetic constants and a hyperbolic dependence of the partition ratio on the hydroxylamine concentration, could be explained by postulating a compulsory isomerisation of the acyl-enzyme intermediate prior to the transfer reaction.

Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa --enzymology--EN; Acetamides; Acetic Acids--pharmacology--PD; Acylation; Amides; Amidohydrolases--antagonists and inhibitors--AI; Binding Sites; Hydrolysis; Hydroxylamines--pharmacology--PD; Kinetics; Models, Chemical; Propionates

CAS Registry No.: 0 (Acetamides); 0 (Acetic Acids); 0 (Amides); 0 (Hydroxylamines); 0 (Propionates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

2/9/16 (Item 16 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

04287097 PMID: 932686

Regulatory properties of an inducible aliphatic amidase **in a thermophilic bacillus.**

Thalenfeld B; Grossowicz N

Journal of general microbiology (ENGLAND) May 1976, 94 (1) p131-41, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

A thermophilic bacillus growing on acetamide as both carbon and nitrogen sources produces an inducible amidase. This amidase hydrolysed the following amides in decreasing order or activity, in comparison with acetamide (1.00): propionamide (0.97), fluoroacetamide (0.84), formamide (0.35) and glycinamide (0.12). Cyanoacetamide, dimethylacetamide, dimethylformamide and urea also induced the synthesis of the amidase, but were not substrates of the enzyme. Studies with protoplasts suggest that the amidase is located in the cytoplasm. Glucose strongly inhibited amidase synthesis; and limiting nitrogen did not release this inhibition. Urea strongly inhibited amidase activity in a competitive manner; but the inhibition caused by iodoacetamide and cyanoacetamide was non-competitive. Both thioacetamide and thiourea were effective inhibitors of enzyme induction. Bacteria grown on a succinate-minimal medium exhibited a lag in amidase synthesis, which could be eliminated by decreasing the concentration of succinate. Acetate- or pyruvate-grown cultures behaved similarly, while those grown on alanine or glutamate exhibited no lag in enzyme induction. In the mutant strain E21, repression of amidase synthesis by glucose was much less evident and no lag for induction was apparent with any of the other carbon sources mentioned.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacillus--enzymology --EN; Acetamides--metabolism--ME; Amides--metabolism--ME; Amidohydrolases --metabolism--ME; Bacillus--growth and development--GD; Bacillus --metabolism--ME; Cell-Free System; Cytoplasm--enzymology--EN; Enzyme Induction--drug effects--DE; Enzyme Repression; Glucose--pharmacology--PD; Heat; Kinetics; Protoplasts--enzymology--EN; Thioacetamide--pharmacology --PD; Thiourea--pharmacology--PD; Urea--pharmacology--PD

CAS Registry No.: 0 (Acetamides); 0 (Amides); 50-99-7 (Glucose); 57-13-6 (Urea); 62-55-5 (Thioacetamide); 62-56-6 (Thiourea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19760823

Record Date Completed: 19760823

2/9/19 (Item 19 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

03398192 PMID: 4625925

Biochemical and immunological comparison of aliphatic amidases **produced by Pseudomonas species.**

Clarke P H

Journal of general microbiology (ENGLAND) Jul 1972, 71 (2) p241-57, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas--enzymology --EN; Acetamides--metabolism--ME; Antigens; Cell-Free System; Cross Reactions; Culture Media; Electrophoresis, Starch Gel; Enzyme Induction; Formamides--metabolism--ME; Genes, Regulator; Genes, Structural; Hydrolases --analysis--AN; Hydrolysis; Immune Sera; Immunodiffusion; Mutation; Phenotype; Pseudomonas--metabolism--ME; Pseudomonas aeruginosa--enzymology --EN; Pseudomonas aeruginosa--immunology--IM; Transferases--analysis--AN

CAS Registry No.: 0 (Acetamides); 0 (Antigens); 0 (Culture Media); 0 (Formamides); 0 (Immune Sera)

Enzyme No.: EC 2. (Transferases); EC 3. (Hydrolases); EC 3.5. (Amidohydrolases)

Record Date Created: 19720922

Record Date Completed: 19720922

2/9/22 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

0011231256 BIOSIS NO.: 199800025503
The aliphatic amidase **: Another way to produce ammonia in H. pylori?**
AUTHOR: Skouloubris S; Labigne A; De Reuse H
AUTHOR ADDRESS: Inst. Pasteur, Paris, France**France
JOURNAL: Gut 41 (SUPPL. 1): pA14 1997 1997
MEDIUM: print
CONFERENCE/MEETING: European Helicobacter Pylori Study Group Xth International Workshop on Gastroduodenal Pathology and Helicobacter Pylori Lisbon, Portugal September 11-14, 1997; 19970911
SPONSOR: European Helicobacter pylori Study Group
ISSN: 0017-5749
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English
REGISTRY NUMBERS: 7664-41-7: ammonia
DESCRIPTORS:
MAJOR CONCEPTS: Enzymology--Biochemistry and Molecular Biophysics; Molecular Genetics--Biochemistry and Molecular Biophysics
BIOSYSTEMATIC NAMES: Aerobic Helical or Vibrioid Gram-Negatives--Eubacteria, Bacteria, Microorganisms
ORGANISMS: Helicobacter-pylori (Aerobic Helical or Vibrioid Gram-Negatives)
COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: aliphatic amidase; ammonia--metabolic production pathways
MISCELLANEOUS TERMS: Meeting Abstract; Meeting Abstract
CONCEPT CODES:
31500 Genetics of bacteria and viruses
10050 Biochemistry methods - General
10054 Biochemistry methods - Proteins, peptides and amino acids
10808 Enzymes - Physiological studies
13002 Metabolism - General metabolism and metabolic pathways
13012 Metabolism - Proteins, peptides and amino acids
31000 Physiology and biochemistry of bacteria
00520 General biology - Symposia, transactions and proceedings
10060 Biochemistry studies - General
10064 Biochemistry studies - Proteins, peptides and amino acids
36002 Medical and clinical microbiology - Bacteriology
BIOSYSTEMATIC CODES:
06210 Aerobic Helical or Vibrioid Gram-Negatives

2/9/45 (Item 1 from file: 65)
DIALOG(R)File 65:Inside Conferences

03333046 INSIDE CONFERENCE ITEM ID: CN035225547
Identification of an aliphatic amidase **in H. pylori**
de Reuse, H.; Skouloubris, S.; Labigne, A.
CONFERENCE: Campylobacter, heliobacter & related organisms-International workshop; 9th
P: 490
Institute of Child Health, 1998
ISBN: 0620216794
LANGUAGE: English DOCUMENT TYPE: Conference Papers
CONFERENCE EDITOR(S): Lastovica, A. J.; Newell, D. G.; Lastovica, E. E.
CONFERENCE SPONSOR: University of Cape Town
CONFERENCE LOCATION: Cape Town
CONFERENCE DATE: Sep 1997 (199709) (199709)

BRITISH LIBRARY ITEM LOCATION: m00/31914
DESCRIPTORS: campylobacter; heliobacter; organisms; child health
?t s2/3,kwic/36 37 39 40 41 43 44 48
>>>KWIC option is not available in file(s): 399

2/3,KWIC/36 (Item 2 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

0230013 DBR Accession No.: 99-00114 PATENT
New Helicobacter sp. aliphatic amidase **AmiE polypeptides and their encoding sequence - Helicobacter pylori recombinant protein preparation, vector expression in host cell and DNA probe and monoclonal antibody, used for infection diagnosis, recombinant vaccine or therapy**
AUTHOR: de Reuse H; Skouloubris S; Labigne A
CORPORATE SOURCE: Paris, France.
PATENT ASSIGNEE: Inst.Pasteur-Paris; INSERM 1998
PATENT NUMBER: WO 9844094 PATENT DATE: 981008 WPI ACCESSION NO.: 98-557106 (9847)
PRIORITY APPLIC. NO.: US 41745 APPLIC. DATE: 970328
NATIONAL APPLIC. NO.: WO 98EP1824 APPLIC. DATE: 980327
LANGUAGE: English

New Helicobacter sp. aliphatic amidase **AmiE polypeptides and their encoding sequence**

2/3,KWIC/37 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0203740 DBR Accession No.: 96-14511
Utilization of acetonitrile and other aliphatic **nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and** amidase **activity**
AUTHOR: Linardi V R; Dias J C T; Rosa C A
CORPORATE AFFILIATE: Univ.Minas-Gerais-Fed.Inst.Biol.Sci.
CORPORATE SOURCE: Departamento de Microbiologia, Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais, C.P. 486, Belo Horizonte, MG 31270-901, Brazil.
JOURNAL: FEMS Microbiol.Lett. (144, 1, 67-71) 1996
ISSN: 0378-1097 CODEN: FMLED7
LANGUAGE: English

Utilization of acetonitrile and other aliphatic **nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and** amidase **activity**

2/3,KWIC/39 (Item 1 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

3528971 0122998
C/HELICOBACTER ALIPHATIC AMIDASE **AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES; SCREENING BY CONTACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES**
Inventors: De Reuse Hilde (FR); Labigne Agnes (FR); Skouloubris Stephane (FR)
Assignee: Institut Pasteur FR
Assignee Code: 42312

	Publication		Application	
Kind	Number	Date	Number	Date
B	US 6248551	20010619	US 9827900	19980223
Priority Applic:			US 9827900	19980223
Provisional Applic:			US 60-41745	19970328

Calculated Expiration: 20180223

HELICOBACTER ALIPHATIC AMIDASE **AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES...**

2/3,KWIC/40 (Item 2 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

3168988 9921350
C/PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITILES; ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND** AMIDASE **ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**
Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John Edward (US); Herkes Frank Edward (US)
Assignee: Du Pont de Nemours, E I & Co
Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5922589	19990713	US 98108729	19980701
Division of:		US 5858736		US 96650073	19960517
Priority Applic:				US 98108729	19980701
				US 96650073	19960517

Calculated Expiration: 20160517

PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITILES...**
...ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE **ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**

2/3,KWIC/41 (Item 3 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

3096789 9901716
C/PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITRILES; CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING** ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**
Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John Edward (US); Herkes Frank Edward (US)
Assignee: Du Pont de Nemours, E I & Co
Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5858736	19990112	US 96650073	19960517
Priority Applic:				US 96650073	19960517

Calculated Expiration: 20160517
CERTIFICATE OF CORRECTION: 19990928

PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITRILES...**
...CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**

2/3,KWIC/43 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.

4166734
Derwent Accession: 1998-041747
Utility

C/ **Preparation of lactams from** aliphatic **[alpha],[omega]-Dinitiles**
; ISOLATED **COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND** AMIDASE **ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**
Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE
Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5922589	A	19990713	US 98108729	19980701
Division	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 19383

Preparation of lactams from aliphatic **[alpha],[omega]-Dinitiles**

2/3,KWIC/44 (Item 3 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4095232
Derwent Accession: 1998-041747
Utility
CERTIFICATE OF CORRECTION
C/ **Preparation of lactams from** aliphatic **[alpha],[omega]-dinitriles**
; CONTACTIN **G DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING** ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**
Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE
Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 20552

Preparation of lactams from aliphatic **[alpha],[omega]-dinitriles**

2/3,KWIC/48 (Item 1 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT
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00453630
i(HELICOBACTER) ALIPHATIC AMIDASE **POLYPEPTIDES, DNA SEQUENCES ENCODING THOSE POLYPEPTIDES AND USES THEREOF**
POLYPEPTIDES DE L' AMIDASE **ALIPHATIQUE AmiE D'i(HELICOBACTER)ET SEQUENCES D'ADN CODANT LESDITS POLYPEPTIDES**
Patent Applicant/Assignee:
INSTITUT PASTEUR,
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE,
DE REUSE Hilde,
SKOULOUBRIS Stephane,

LABIGNE Agnes,
Inventor(s):
DE REUSE Hilde,
SKOULOUBRIS Stephane,
LABIGNE Agnes,
Patent and Priority Information (Country, Number, Date):
Patent: WO 9844094 A2 19981008
Application: WO 98EP1824 19980327 (PCT/WO EP9801824)
Priority Application: US 9741745 19970328
Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW GH GM KE LS MW SD SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN ML MR NE SN TD TG
Publication Language: English
Fulltext Word Count: 9017

i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING THOSE POLYPEPTIDES AND USES THEREOF
POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE AmiE D'i(HELICOBACTER)ET SEQUENCES D'ADN CODANT LESDITS POLYPEPTIDES

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$1.60 1 Types

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     $22.06   Estimated total session cost    0.577 DialUnits

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      $0.02   TELNET
      $1.03   Estimated cost this search
      $1.03   Estimated total session cost   0.162 DialUnits

File 155:MEDLINE(R)  1966-2004/Apr W1
       (c) format only 2004 The Dialog Corp.
*File 155: Medline has been reloaded. Accession numbers
have changed. Please see HELP NEWS 154 for details.

       Set  Items  Description
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?s aliphatic? (3n) amidase?
             6440  ALIPHATIC?
             2018  AMIDASE?
       S1      42  ALIPHATIC? (3N) AMIDASE?
?s s1/1998:2004
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          3111437  PY=1998 : PY=2004
       S2      12  S1/1998:2004
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               42  S1
               12  S2
       S3      30  S1 NOT S2
?t s3/9/all

 3/9/1
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

13675690   PMID: 9364923
   Identification and characterization of an aliphatic amidase in
Helicobacter pylori.
  Skouloubris S; Labigne A; De Reuse H
  Unite de Pathogenie Bacterienne des Muqueuses, Institut Pasteur, Paris,
France.
  Molecular microbiology (ENGLAND)  Sep 1997,  25  (5)  p989-98, ISSN
0950-382X  Journal Code: 8712028
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Subfile:  INDEX MEDICUS
  We report, for the first time, the presence in Helicobacter pylori of an
 aliphatic amidase that, like urease, contributes to ammonia production.
 Aliphatic amidases are cytoplasmic acylamide amidohydrolases (EC
3.5.1.4) hydrolysing short-chain aliphatic amides to produce ammonia and
the corresponding organic acid. The finding of an aliphatic amidase in
H. pylori was unexpected as this enzyme has only previously been described
in bacteria of environmental (soil or water) origin. The H. pylori amidase
gene amiE (1017 bp) was sequenced, and the deduced amino acid sequence of
AmiE (37746Da) is very similar (75% identity) to the other two sequenced
 aliphatic amidases , one from Pseudomonas aeruginosa and one from
Rhodococcus sp. R312. Amidase activity was measured as the release of
ammonia by sonicated crude extracts from H. pylori strains and from
recombinant Escherichia coli strains overproducing the H. pylori amidase.
The substrate specificity was analysed with crude extracts from H. pylori
cells grown in vitro; the best substrates were propionamide, acrylamide and
acetamide. Polymerase chain reaction (PCR) amplification of an internal
amiE sequence was obtained with each of 45 different H. pylori clinical
isolates, suggesting that amidase is common to all H. pylori strains. A H.
pylori mutant (N6-836) carrying an interrupted amiE gene was constructed by
allelic exchange. No amidase activity could be detected in N6-836. In a
N6-urease negative mutant, amidase activity was two- to threefold higher
than in the parental strain N6. Crude extracts of strain N6 slowly
hydrolysed formamide. This activity was affected in neither the amidase
negative strain (N6-836) nor a double mutant strain deficient in both
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amidase and urease activities, suggesting the presence of an independent discrete formamidase in H. pylori. The existence of an **aliphatic amidase**, a correlation between the urease and amidase activities and the possible presence of a formamidase indicates that H. pylori has a large range of possibilities for intracellular ammonia production.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; *Helicobacter pylori --enzymology--EN; Amino Acid Sequence; Cloning, Molecular; DNA, Recombinant ; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Genes, Structural, Bacterial--genetics--GE; Helicobacter pylori--chemistry--CH; Helicobacter pylori--genetics--GE; Molecular Sequence Data; Mutation --genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins --metabolism--ME; Sequence Homology, Amino Acid; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/Y12252

CAS Registry No.: 0 (DNA, Recombinant); 0 (Recombinant Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19980129

Record Date Completed: 19980129

3/9/2

DIALOG(R)File 155:MEDLINE(R)

13022578 PMID: 8662959

A novel gene cluster including the Rhodococcus rhodochrous J1 nhlBA genes encoding a low molecular mass nitrile hydratase (L-NHase) induced by its reaction product.

Komeda H; Kobayashi M; Shimizu S

Department of Agricultural Chemistry, Faculty of Agriculture, Kyoto University, Kyoto 606-01, Japan.

Journal of biological chemistry (UNITED STATES) Jun 28 1996, 271 (26) p15796-802, ISSN 0021-9258 Journal Code: 2985121R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The 3.5 kilobases (kb) of the 5'-upstream region from nhlBA encoding a cobalt-containing low molecular mass nitrile hydratase (L-NHase) from Rhodococcus rhodochrous J1 was found to be required for the amide-dependent expression of nhlBA in experiments using a Rhodococcus transformation system. Sequence analysis of the 3.5-kb fragment revealed the presence of two open reading frames (nhlD and nhlC) in this fragment. NhlD has similarity to regulators MerR, CadC, and ArsR. NhlC has similarity to the regulators AmiC, for the expression of an **aliphatic amidase** from Pseudomonas aeruginosa, and NhhC, for the expression of a high molecular mass nitrile hydratase from R. rhodochrous J1. Assays of NHase activity of transformants carrying nhlD deletion or nhlC deletion mutations suggest a negative regulatory role for nhlD and a positive regulatory role for nhlC in the process of the L-NHase formation. Assays of NHase and amidase activities and Western blot analyses of each Rhodococcus transformant carrying various deletion plasmids, have shown that nhlBA and amdA encoding an amidase, which is located 1.9 kb downstream of nhlBA, were regulated in the same manner. These findings present the genetic evidence for a novel gene cluster controlling the expression of L-NHase, which is induced by the reaction product (amide) in the "practical microorganism" R. rhodochrous J1.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Gene Expression Regulation, Bacterial; *Genes, Structural, Bacterial; *Hydro-Lyases--genetics--GE; *Nitriles--metabolism--ME; *Rhodococcus--genetics--GE; Base Sequence; Cloning, Molecular; DNA, Bacterial--genetics--GE; Gene Expression Regulation, Bacterial --drug effects--DE; Gene Expression Regulation, Enzymologic--drug effects--DE; Molecular Sequence Data; Molecular Weight; Open Reading Frames; RNA, Messenger--genetics--GE; Restriction Mapping; Sequence Alignment; Sequence Homology, Amino Acid

Molecular Sequence Databank No.: GENBANK/D67028

CAS Registry No.: 0 (DNA, Bacterial); 0 (Nitriles); 0 (RNA,

Messenger)
Enzyme No.: EC 4.2.1. (Hydro-Lyases); EC 4.2.1.- (nitrile hydratase)
Record Date Created: 19960820
Record Date Completed: 19960820

3/9/3
DIALOG(R)File 155:MEDLINE(R)

12684768 PMID: 7607322
Pseudomonas aeruginosa aliphatic amidase **is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.**
Novo C; Tata R; Clemente A; Brown P R
Instituto Nacional de Engenharia e Tecnologia Industrial/IBQTA, Queluz, Portugal.
FEBS letters (NETHERLANDS) Jul 3 1995, 367 (3) p275-9, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A database search indicated homology between some members of the nitrilase/cyanide hydratase family, Pseudomonas aeruginosa and Rhodococcus erythropolis amidases and several other proteins, some of unknown function. BLOCK and PROFILE searches confirmed these relationships and showed that four regions of the P. aeruginosa amidase had significant homology with corresponding regions of nitrilases. A phylogenetic tree placed the P. aeruginosa and R. erythropolis amidases in a group with nitrilases but separated other amidases into three groups. The active site cysteine in nitrilases is conserved in the P. aeruginosa amidase indicating that Cys166 is the active site nucleophile.
Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--chemistry--CH; *Pseudomonas aeruginosa --enzymology--EN; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Binding Sites; Cysteine--chemistry--CH; Hydro-Lyases--chemistry--CH; Molecular Sequence Data; Phylogeny; Sequence Alignment; Sequence Homology, Amino Acid
CAS Registry No.: 52-90-4 (Cysteine)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)
Record Date Created: 19950817
Record Date Completed: 19950817

3/9/4
DIALOG(R)File 155:MEDLINE(R)

10289814 PMID: 7987228
A new family of carbon-nitrogen hydrolases.
Bork P; Koonin E V
European Molecular Biology Laboratory, Heidelberg, Germany.
Protein science - a publication of the Protein Society (UNITED STATES) Aug 1994, 3 (8) p1344-6, ISSN 0961-8368 Journal Code: 9211750
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Using computer methods for database search and multiple alignment, statistically significant sequence similarities were identified between several nitrilases with distinct substrate specificity, cyanide hydratases, **aliphatic amidases**, beta-alanine synthase, and a few other proteins with unknown molecular function. All these proteins appear to be involved in the reduction of organic nitrogen compounds and ammonia production.

Sequence conservation over the entire length, as well as the similarity in the reactions catalyzed by the known enzymes in this family, points to a common catalytic mechanism. The new family of enzymes is characterized by several conserved motifs, one of which contains an invariant cysteine that is part of the catalytic site in nitrilases. Another highly conserved motif includes an invariant glutamic acid that might also be involved in catalysis.

Tags: Comparative Study

Descriptors: *Hydrolases--chemistry--CH; *Sequence Alignment; Amidohydrolases--chemistry--CH; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Aminohydrolases--metabolism --ME; Ammonia--pharmacology--PD; Databases, Factual; Hydro-Lyases --chemistry--CH; Hydro-Lyases--metabolism--ME; Hydrolases--metabolism--ME; Information Storage and Retrieval; Molecular Sequence Data; Open Reading Frames; Sequence Homology

Molecular Sequence Databank No.: GENBANK/X52543; GENBANK/X66132; GENBANK/Z14933

CAS Registry No.: 7664-41-7 (Ammonia)

Enzyme No.: EC 3. (Hydrolases); EC 3.5. (Amidohydrolases); EC 3.5.1.6 (beta-ureidopropionase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)

Record Date Created: 19950111

Record Date Completed: 19950111

3/9/5

DIALOG(R)File 155:MEDLINE(R)

10242343 PMID: 7944367

Purification and characterization of an amidase from an acrylamide-degrading Rhodococcus sp.

Nawaz M S; Khan A A; Seng J E; Leakey J E; Siitonen P H; Cerniglia C E

Division of Microbiology, National Center for Toxicological Research, Food and Drug Administration, Jefferson, Arkansas 72079.

Applied and environmental microbiology (UNITED STATES) Sep 1994, 60 (9) p3343-8, ISSN 0099-2240 Journal Code: 7605801

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A constitutively expressed **aliphatic amidase** from a Rhodococcus sp. catalyzing acrylamide deamination was purified to electrophoretic homogeneity. The molecular weight of the native enzyme was estimated to be 360,000. Upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis, the purified preparation yielded a homogeneous protein band having an apparent molecular weight of about 44,500. The amidase had pH and temperature optima of 8.5 and 40 degrees C, respectively, and its isoelectric point was pH 4.0. The amidase had apparent K(m) values of 1.2, 2.6, 3.0, 2.7, and 5.0 mM for acrylamide, acetamide, butyramide, propionamide, and isobutyramide, respectively. Inductively coupled plasma-atomic emission spectometry analysis indicated that the enzyme contains 8 mol of iron per mol of the native enzyme. No labile sulfide was detected. The amidase activity was enhanced by, but not dependent on Fe(2+), Ba(2+), and Cr(2+). However, the enzyme activity was partially inhibited by Mg(2+) and totally inhibited in the presence of Ni(2+), Hg(2+), Cu(2+), Co(2+), specific iron chelators, and thiol blocking reagents. The NH2-terminal sequence of the first 18 amino acids displayed 88% homology to the **aliphatic amidase** of Brevibacterium sp. strain R312.

Descriptors: *Acrylamides--metabolism--ME; *Amidohydrolases --isolation and purification--IP; *Rhodococcus--metabolism--ME; Acrylamide; Amidohydrolases--chemistry--CH; Amidohydrolases--genetics--GE; Amino Acid Sequence; Amino Acids--analysis--AN; Biodegradation; Isoelectric Point; Kinetics; Metals--pharmacology--PD; Molecular Sequence Data; Molecular Weight; Rhodococcus--genetics--GE; Rhodococcus--isolation and purification --IP; Substrate Specificity; Temperature

CAS Registry No.: 0 (Acrylamides); 0 (Amino Acids); 0 (Metals);

79-06-1 (Acrylamide)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19941118
Record Date Completed: 19941118

3/9/6
DIALOG(R)File 155:MEDLINE(R)

10160827 PMID: 8051020
Identification and structure of the nasR gene encoding a nitrate- and nitrite-responsive positive regulator of nasFEDCBA (nitrate assimilation) operon expression in Klebsiella pneumoniae M5al.
Goldman B S; Lin J T; Stewart V
Sections of Microbiology, Cornell University, Ithaca, New York 14853-8101.
Journal of bacteriology (UNITED STATES) Aug 1994, 176 (16) p5077-85, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Klebsiella pneumoniae can use nitrate and nitrite as sole nitrogen sources through the nitrate assimilatory pathway. The structural genes for assimilatory nitrate and nitrite reductases together with genes necessary for nitrate transport form an operon, nasFEDCBA. Expression of the nasF operon is regulated both by general nitrogen control and also by nitrate or nitrite induction. We have identified a gene, nasR, that is necessary for nitrate and nitrite induction. The nasR gene, located immediately upstream of the nasFEDCBA operon, encodes a 44-kDa protein. The NasR protein shares carboxyl-terminal sequence similarity with the AmiR protein of Pseudomonas aeruginosa, the positive regulator of amiE (**aliphatic amidase**) gene expression. In addition, we present evidence that the nasF operon is not autogenously regulated.
Tags: Support, U.S. Gov't, Non-P.H.S.
Descriptors: *Gene Expression Regulation, Bacterial; *Genes, Regulator; *Genes, Structural, Bacterial; *Klebsiella pneumoniae--genetics--GE; *Nitrates--metabolism--ME; *Nitrites--metabolism--ME; *Trans-Activators --genetics--GE; Amino Acid Sequence; Base Sequence; DNA-Binding Proteins --metabolism--ME; Molecular Sequence Data; Mutagenesis, Insertional; Operon ; Trans-Activation (Genetics)
Molecular Sequence Databank No.: GENBANK/L27824
CAS Registry No.: 0 (DNA-Binding Proteins); 0 (Nitrates); 0 (Nitrites); 0 (Trans-Activators); 0 (nasR protein)
Gene Symbol: amiR; nadB; nasA; nasC; nasD; nasE; nasF; nasR
Record Date Created: 19940907
Record Date Completed: 19940907

3/9/7
DIALOG(R)File 155:MEDLINE(R)

09908517 PMID: 8253087
Antitermination of amidase expression in Pseudomonas aeruginosa is controlled by a novel cytoplasmic amide-binding protein.
Wilson S A; Wachira S J; Drew R E; Jones D; Pearl L H
Biomolecular Structure Group, University College London, UK.
EMBO journal (ENGLAND) Sep 1993, 12 (9) p3637-42, ISSN 0261-4189 Journal Code: 8208664
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Amide-inducible expression of the **aliphatic amidase** system of Pseudomonas aeruginosa can be reconstituted in Escherichia coli with only

the amidase structural gene amiE, the negative regulator amiC and the positive regulator amiR, a transcription antitermination factor. Complementation experiments in E. coli suggest that negative control of amidase expression by AmiC is mediated by a protein-protein interaction with AmiR. Purified AmiC binds acetamide with a KD of 3.7 microM in equilibrium dialysis studies, and therefore AmiC appears to be the sensory partner of the AmiC/AmiR pair of regulatory proteins, responding to the presence of amides. Sequence analysis techniques suggest that AmiC is a member of the structural family of periplasmic binding proteins, but has a distinct and novel cytoplasmic role.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacterial Proteins --metabolism--ME; *Gene Expression Regulation, Bacterial; *Gene Expression Regulation, Enzymologic; *Genes, Bacterial; *Periplasmic Binding Proteins; *Pseudomonas aeruginosa--enzymology--EN; *Repressor Proteins--metabolism --ME; Amidohydrolases--genetics--GE; Amino Acid Sequence; Bacterial Proteins--biosynthesis--BI; Consensus Sequence; Genes, Regulator; Genes, Structural, Bacterial; Genetic Complementation Test; Kinetics; Molecular Sequence Data; Operon; Protein Structure, Secondary; Pseudomonas aeruginosa --metabolism--ME; Restriction Mapping; Sequence Homology, Amino Acid

CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Repressor Proteins); 142462-53-1 (AmiC protein, Pseudomonas aeruginosa)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Gene Symbol: amiB; amiC; amiE; amiR; amiS

Record Date Created: 19940110

Record Date Completed: 19940110

3/9/8

DIALOG(R)File 155:MEDLINE(R)

09774423 PMID: 8336670

Structural, functional, and evolutionary relationships among extracellular solute-binding receptors of bacteria.

Tam R; Saier M H

Department of Biology, University of California, San Diego, La Jolla 92093-0116.

Microbiological reviews (UNITED STATES) Jun 1993, 57 (2) p320-46, ISSN 0146-0749 Journal Code: 7806086

Contract/Grant No.: 2RO1AI14176; AI; NIAID; 5RO1AI21702; AI; NIAID

Document type: Journal Article; Review; Review, Academic

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Extracellular solute-binding proteins of bacteria serve as chemoreceptors, recognition constituents of transport systems, and initiators of signal transduction pathways. Over 50 sequenced periplasmic solute-binding proteins of gram-negative bacteria and homologous extracytoplasmic lipoproteins of gram-positive bacteria have been analyzed for sequence similarities, and their degrees of relatedness have been determined. Some of these proteins are homologous to cytoplasmic transcriptional regulatory proteins of bacteria; however, with the sole exception of the vitamin B12-binding protein of Escherichia coli, which is homologous to human glutathione peroxidase, they are not demonstrably homologous to any of the several thousand sequenced eukaryotic proteins. Most of these proteins fall into eight distinct clusters as follows. Cluster 1 solute-binding proteins are specific for malto-oligosaccharides, multiple oligosaccharides, glycerol 3-phosphate, and iron. Cluster 2 proteins are specific for galactose, ribose, arabinose, and multiple monosaccharides, and they are homologous to a number of transcriptional regulatory proteins including the lactose, galactose, and fructose repressors of E. coli. Cluster 3 proteins are specific for histidine, lysine-arginine-ornithine, glutamine, octopine, nopaline, and basic amino acids. Cluster 4 proteins are specific for leucine and leucine-isoleucine-valine, and they are homologous to the **aliphatic amidase** transcriptional repressor, AmiC, of Pseudomonas aeruginosa.

Cluster 5 proteins are specific for dipeptides and oligopeptides as well as nickel. Cluster 6 proteins are specific for sulfate, thiosulfate, and possibly phosphate. Cluster 7 proteins are specific for dicarboxylates and tricarboxylates, but these two proteins exhibit insufficient sequence similarity to establish homology. Finally, cluster 8 proteins are specific for iron complexes and possibly vitamin B12. Members of each cluster of binding proteins exhibit greater sequence conservation in their N-terminal domains than in their C-terminal domains. Signature sequences for these eight protein families are presented. The results reveal that binding proteins specific for the same solute from different bacteria are generally more closely related to each other than are binding proteins specific for different solutes from the same organism, although exceptions exist. They also suggest that a requirement for high-affinity solute binding imposes severe structural constraints on a protein. The occurrence of two distinct classes of bacterial cytoplasmic repressor proteins which are homologous to two different clusters of periplasmic binding proteins suggests that the gene-splicing events which allowed functional conversion of these proteins with retention of domain structure have occurred repeatedly during evolutionary history.(ABSTRACT TRUNCATED AT 400 WORDS) (227 Refs.)

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Bacteria--metabolism--ME; *Bacterial Proteins--analysis--AN ; *Carrier Proteins--analysis--AN; Amino Acid Sequence; Bacterial Proteins --chemistry--CH; Biological Transport; Carrier Proteins--chemistry--CH; Carrier Proteins--physiology--PH; Evolution; Molecular Sequence Data; Structure-Activity Relationship

CAS Registry No.: 0 (Bacterial Proteins); 0 (Carrier Proteins)

Record Date Created: 19930824

Record Date Completed: 19930824

3/9/9

DIALOG(R)File 155:MEDLINE(R)

09368661 PMID: 1628849

Cloning and primary structure of the wide-spectrum amidase from Brevibacterium sp. R312: high homology to the amiE product from Pseudomonas aeruginosa.

Soubrier F; Levy-Schil S; Mayaux J F; Petre D; Arnaud A; Crouzet J

Departement Biotechnologie, Rhone-Poulenc Rorer, Centre de Recherche de Vitry-Alfortville, Vitry sur Seine, France.

Gene (NETHERLANDS) Jul 1 1992, 116 (1) p99-104, ISSN 0378-1119 Journal Code: 7706761

Erratum in Gene 1993 Feb 28;124(2) 309

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A Brevibacterium sp. R312 DNA fragment encoding the wide-spectrum amidase (EC 3.5.1.4) has been cloned and sequenced, using limited amino acid (aa) sequence information obtained from the purified enzyme. The deduced aa sequence showed more than 80% strict identity with the Pseudomonas aeruginosa **aliphatic amidase** , the product of the amiE gene, suggesting a horizontal transfer of the gene during evolution between Gram+ and Gram- bacteria.

Descriptors: *Amidohydrolases--genetics--GE; *Brevibacterium--enzymology --EN; *Escherichia coli--genetics--GE; *Pseudomonas aeruginosa--enzymology --EN; Amidohydrolases--chemistry--CH; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Base Sequence; Brevibacterium--genetics--GE; Cloning, Molecular; Escherichia coli--enzymology--EN; Molecular Sequence Data; Pseudomonas aeruginosa--genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins--metabolism--ME; Restriction Mapping

Molecular Sequence Databank No.: GENBANK/M74890; GENBANK/M74891; GENBANK/M74892; GENBANK/M76451; GENBANK/M77131; GENBANK/M77132; GENBANK/M79309; GENBANK/M79310; GENBANK/S38798; GENBANK/S38799

CAS Registry No.: 0 (Recombinant Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Gene Symbol: amiE

Record Date Created: 19920817
Record Date Completed: 19920817

3/9/10
DIALOG(R)File 155:MEDLINE(R)

09284651 PMID: 1368108
N-terminal amino acid sequence of Brevibacterium sp. R312 wide-spectrum amidase.
Chion C K; Duran R; Arnaud A; Galzy P
Chaire de Microbiologie Industrielle et de Genetique des Microorganismes, Ecole Nationale Superieure Agronomique de Montpellier, France.
Applied microbiology and biotechnology (GERMANY) Nov 1991, 36 (2) p205-7, ISSN 0175-7598 Journal Code: 8406612
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: BIOTECHNOLOGY
A wide-spectrum amidase from Brevibacterium sp. R312 was partially purified. The enzyme subunit was purified by reversed phase HPLC and the N-terminal amino acid sequence was found to be identical to that of Pseudomonas aeruginosa **aliphatic amidase** .
Tags: Comparative Study
Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins --genetics--GE; *Brevibacterium--enzymology--EN; Amidohydrolases--isolation and purification--IP; Amino Acid Sequence; Bacterial Proteins--isolation and purification--IP; Brevibacterium--genetics--GE; Chromatography, High Pressure Liquid; Molecular Sequence Data; Pseudomonas aeruginosa--genetics --GE; Sequence Homology, Nucleic Acid; Species Specificity
CAS Registry No.: 0 (Bacterial Proteins)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19920611
Record Date Completed: 19920611

3/9/11
DIALOG(R)File 155:MEDLINE(R)

08977358 PMID: 1907262
Cloning and DNA sequence of amiC, a new gene regulating expression of the Pseudomonas aeruginosa aliphatic amidase **, and purification of the amiC product.**
Wilson S; Drew R
Department of Biochemistry, University College London, United Kingdom.
Journal of bacteriology (UNITED STATES) Aug 1991, 173 (16) p4914-21, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Using in vitro-constructed deletions and subcloned DNA fragments, we have identified a new gene, amiC, which regulates expression of the inducible Pseudomonas aeruginosa **aliphatic amidase** activity. The DNA sequence of the gene has been determined, and an open reading frame encoding a polypeptide of 385 amino acids (molecular mass, 42,834 Da) has been identified. A search of sequence libraries has failed to find homologies with other published sequences. The amiC translation termination codon (A)TGA overlaps the initiation codon for the downstream amiR transcription antitermination factor gene, implying that the amiCR operon is coordinately regulated. Disruption of the amiC open reading frame by insertion and deletion leads to constitutive amidase synthesis, suggesting that AmiC is a negative regulator. This is confirmed by the finding that a broad-host-range expression vector carrying amiC (pSW41) represses amidase expression in a series of previously characterized P. aeruginosa

amidase-constitutive mutants. The AmiC polypeptide has been purified from PAC452(pSW41), and N-terminal amino acid sequencing has confirmed the gene identification.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins --isolation and purification--IP; *Genes, Regulator--genetics--GE; *Periplasmic Binding Proteins; *Pseudomonas aeruginosa--genetics--GE; *Repressor Proteins--isolation and purification--IP; Amidohydrolases --biosynthesis--BI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Base Sequence; Enzyme Induction; Escherichia coli--metabolism--ME; Gene Expression Regulation, Bacterial; Molecular Sequence Data; Mutation --genetics--GE; Plasmids--genetics--GE; Pseudomonas aeruginosa--enzymology --EN; Repressor Proteins--genetics--GE; Restriction Mapping
Molecular Sequence Databank No.: GENBANK/M43175; GENBANK/M74478; GENBANK/M74479; GENBANK/M74480; GENBANK/M74481; GENBANK/M74482; GENBANK/M74483; GENBANK/M74484; GENBANK/S45931; GENBANK/S45975; GENBANK/X13776
CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Plasmids); 0 (Repressor Proteins); 142462-53-1 (AmiC protein, Pseudomonas aeruginosa)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19910905
Record Date Completed: 19910905

3/9/12
DIALOG(R)File 155:MEDLINE(R)

08374586 PMID: 2513374
Positive control of Pseudomonas aeruginosa amidase synthesis is mediated by a transcription anti-termination mechanism.
Drew R; Lowe N
Department of Biochemistry, University College London, UK.
Journal of general microbiology (ENGLAND) Apr 1989, 135 (Pt 4) p817-23, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The DNA sequence of the region upstream from the amidase structural gene (amiE) of Pseudomonas aeruginosa indicates that amidase (EC 3.5.1.4) is transcribed from an Escherichia coli-like promoter located 150 bp before the amiE translation initiation codon. The sequence between the promoter and the coding sequence includes a single open reading frame followed by an E. coli-like rho-independent transcription terminator. A deletion within the presumed terminator region which disrupts the potential stem/loop formation leads to high constitutive amidase expression which is independent of the product of the regulator gene (amiR). It is proposed that the catabolic **aliphatic amidase** of P. aeruginosa is regulated by a transcription anti-termination mechanism. The magnoconstitutive mutant PAC433 has promoter and terminator sequences identical to the wild-type PAC1 but contains a single base pair change in the amiE gene ribosome-binding site.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas aeruginosa --genetics--GE; *Transcription, Genetic; Amidohydrolases--genetics--GE; Base Sequence; DNA, Bacterial--analysis--AN; Molecular Sequence Data; Plasmids; Pseudomonas aeruginosa--enzymology--EN; Restriction Mapping
Molecular Sequence Databank No.: GENBANK/M25262
CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19900126
Record Date Completed: 19900126

3/9/13
DIALOG(R)File 155:MEDLINE(R)

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08102032 PMID: 2495988
Nucleotide sequence of the aliphatic amidase **regulator gene (amiR) of Pseudomonas aeruginosa.**
Lowe N; Rice P M; Drew R E
Department of Biochemistry, University College London, England.
FEBS letters (NETHERLANDS) Mar 27 1989, 246 (1-2) p39-43, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The nucleotide sequence of a 1001 bp ClaI/XhoI DNA fragment encoding the amidase regulator gene (amiR) from Pseudomonas aeruginosa has been determined. The sequence derives from strain PAC433, a constitutive high expressing amidase mutant, and contains two overlapping open reading frames. Analysis of the sequence has identified one of the reading frames as amiR. The gene encodes a 196 amino acid polypeptide which shows a strong bias towards codons with G or C in the third position. The amiR gene shows no sequence homology with other bacterial regulator proteins.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Regulator; *Pseudomonas aeruginosa--genetics--GE; Amino Acid Sequence; Base Sequence; Codon; Deoxyribonucleases, Type II Site-Specific; Molecular Sequence Data; Molecular Weight; Pseudomonas aeruginosa--enzymology--EN; Translation, Genetic
Molecular Sequence Databank No.: GENBANK/X13776
CAS Registry No.: 0 (Codon)
Enzyme No.: EC 3.1.21.- (endodeoxyribonuclease ClaI); EC 3.1.21.- (endodeoxyribonuclease XhoI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific); EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19890608
Record Date Completed: 19890608

3/9/14
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

07448695 PMID: 3108030
The nucleotide sequence of the amiE gene of Pseudomonas aeruginosa.
Brammar W J; Charles I G; Matfield M; Liu C P; Drew R E; Clarke P H
FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p291-4, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The nucleotide sequence of the amiE gene, encoding the **aliphatic amidase** of Pseudomonas aeruginosa, has been determined. The sequence of 1038 nucleotides shows a strong bias in favour of codons with G or C in the third position, and only 44 different codons are utilised.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Base Sequence; Codon--analysis--AN; DNA, Bacterial--analysis--AN; RNA, Messenger--analysis--AN; Templates, Genetic
CAS Registry No.: 0 (Codon); 0 (DNA, Bacterial); 0 (RNA, Messenger)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19870626
Record Date Completed: 19870626

3/9/15
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

07448694 PMID: 3108029

The amino acid sequence of the aliphatic amidase **from Pseudomonas aeruginosa.**

Ambler R P; Auffret A D; Clarke P H

FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p285-90, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Amino acid sequence studies show that the **aliphatic amidase** (EC 3.5.1.4) from Pseudomonas aeruginosa PAC142 consists of a single polypeptide chain of 346 residues, giving an Mr of 38,400. The evidence from the amino acid studies is in complete agreement with that deduced from the DNA sequence of the amiE gene. Studies of the protein from Pseudomonas putida A87 show that it differs from the Ps. aeruginosa protein by about 30 amino acid substitutions. It now becomes possible to relate changes in the enzyme which result in altered specificity to structural changes in the protein.

Tags: Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; *Pseudomonas aeruginosa --enzymology--EN; Amino Acid Sequence; Peptide Fragments--analysis--AN

CAS Registry No.: 0 (Peptide Fragments)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19870626

Record Date Completed: 19870626

3/9/16

DIALOG(R)File 155:MEDLINE(R)

07316491 PMID: 3098906

A comparative study of acquired amidase activity in Pseudomonas species.

Wyndham R C; Slater J H

Journal of general microbiology (ENGLAND) Aug 1986, 132 (Pt 8) p2195-204, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Pseudomonas putida PP3 carrying dehalogenases I and II and Pseudomonas aeruginosa PAU3 carrying dehalogenase I coded for by plasmid pUU2 were able to grow on 2-monochloropropionic acid (2MCPA). Neither strain utilized 2-chloropropionamide (2CPA) as a carbon or nitrogen source for growth. Mutations in both strains to 2Cpa+ phenotypes (designated P. putida PPW3 and P. aeruginosa PAU5, respectively) involved the expression of an acquired 2CPA-amidase activity. The amidase followed by dehalogenase reactions in these strains constituted a novel metabolic pathway for growth on 2CPA. P. putida PPW3 synthesized a constitutive amidase of molecular mass 59 kDa consisting of two identical subunits of 29 kDa. For those amides tested this acquired enzyme was most active against chlorinated aliphatic amides, although substrate affinities (Km) and maximum rates of activity (Vmax) were poor. P. aeruginosa PAU5 acquired a 2Cpa+ phenotype by overproducing the A-amidase normally used by this species to hydrolyse **aliphatic** amides. The A- **amidase** had only slight activity towards 2CPA. However, with constitutive synthesis the mutant grew on the chlorinated substrates. Chloroacetamide (CAA) was a toxic substrate analogue for these Pseudomonas strains. A strain resistant to CAA was isolated from P. aeruginosa PAU5 when exposed to 1-10 mM-CAA. This mutant, P. aeruginosa PAU6, synthesized an inducible A-amidase. CAA-resistance depended upon the simultaneous expression of CAA-inducible amidase and dehalogenase activities.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Aminohydrolases--metabolism--ME; *Pseudomonas--enzymology --EN; Acetamides--metabolism--ME; Acetyltransferases--metabolism--ME;

Aminohydrolases--isolation and purification--IP; Mutation; Phenotype; Pseudomonas--growth and development--GD; Pseudomonas aeruginosa--enzymology --EN; Pseudomonas aeruginosa--growth and development--GD
CAS Registry No.: 0 (Acetamides); 79-07-2 (chloroacetamide)
Enzyme No.: EC 2.3.1. (Acetyltransferases); EC 3.5.4. (Aminohydrolases)
Record Date Created: 19870219
Record Date Completed: 19870219

3/9/17
DIALOG(R)File 155:MEDLINE(R)

06715270 PMID: 6440948
Complementation analysis of the aliphatic amidase **genes of Pseudomonas aeruginosa.**
Drew R
Journal of general microbiology (ENGLAND) Dec 1984, 130 (Pt 12) p3101-11, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A plasmid, pCL34, capable of autonomous replication in Escherichia coli and Pseudomonas aeruginosa has been constructed which carries the promoter and structural gene (amiE) for P. aeruginosa amidase, but not the regulator gene (amiR). Plasmid pCL34 has been mobilized from E. coli to P. aeruginosa using the broad host range plasmid RP4. Complementation studies were performed in P. aeruginosa strains carrying various amidase mutations. Measurements of amidase activity in the recipients under inducing, non-inducing and repressing conditions showed trans-complementation by the chromosomally located regulator gene product. These results confirmed the positive control model for amidase gene expression. Levels of amidase expression seen during these studies were approximately threefold higher than in the parental, amidase-positive strains.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Chromosome Mapping; Gene Expression Regulation; Genetic Complementation Test; Phenotype; Plasmids; Pseudomonas aeruginosa--enzymology--EN; Transformation, Bacterial
CAS Registry No.: 0 (Plasmids)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19850314
Record Date Completed: 19850314

3/9/18
DIALOG(R)File 155:MEDLINE(R)

05674138 PMID: 6793036
Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase **from Pseudomonas aeruginosa.**
Hollaway M R; Clarke P H; Ticho T
Biochemical journal (ENGLAND) Dec 1 1980, 191 (3) p811-26, ISSN 0264-6021 Journal Code: 2984726R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
1. Chloroacetone (I) was shown to be an active-site-directed inhibitor of the **aliphatic amidase** (EC 3.5.1.4) from Pseudomonas aeruginosa strain PAC142.2. This inhibitor reacted with the enzyme in two stages: the first involving the reversible formation of an enzymically inactive species, EI, and the second the formation of a species, EX, from which enzymic activity could not be recovered. 3. Different types of kinetic experiment were

conducted to test conformity of the reaction to the scheme: E + I k+1 Equilibrium k-1 EI Leads to K+2 EX A computer-based analysis of the results was carried out and values of the individual rate constants were determined. 4. No direct evidence for a binding step before the formation of EI could be obtained, as with [E]0 Less Than [I]0 the observed first-order rate constant for the formation of EI was directly proportional to the concentration of chloroacetone up to 1.2 mM (above this concentration the reaction became too rapid to follow even by the stopped-flow method developed to investigate fast inhibition). 5. The value of k+1 exhibited a bell-shaped pH-dependency with a maximum value of about 3 X 10(3) M-1. S-1 at pH6 and apparent pKa values of 7.8 and about 4.8.6. The values of k-1 and K+2 were similar and changed with the time of reaction from values of about 3 X 10(-3) S-1 (pH8.6) at short times to about one-sixth this value for longer periods of incubation. In this respect the simple reaction scheme is insufficient to describe the inhibition process. 7. The overall inhibition reaction is rapid, whether it is considered in relation to the expected chemical reactivity of chloroacetone, the rate of reaction of other enzymes with substrate analogues containing the chloromethyl group, or the rate of the amidase-catalysed hydrolysis of N-methylacetamide, a substrate that is nearly isosteric with chloroacetone. 8. Acetamide protected the amidase from inhibition by chloroacetone, and the concentration-dependence of the protection gave a value of an apparent dissociation constant similar to the Km value for this substrate. 9. Addition of acetamide to solutions of the species EI led to a slow recovery of activity. Recovery of active enzyme was also observed after dilution of a solution of EI in the absence of substrate. 10. The species EI is considered not to be a simple adsorption complex, and the possibilities are discussed that it may be a tetrahedral carbonyl adduct, a Schiff base (azomethine) or a complex in which the enzyme has undergone a structural change. The species EX is probably a derivative in which there is a covalent bond between a group in the enzyme and the C-1 atom of the inhibitor.

Descriptors: *Acetone--analogs and derivatives--AA; *Amidohydrolases --antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetone--pharmacology--PD; Binding Sites; Kinetics; Models, Chemical

CAS Registry No.: 0 (Acetamides); 67-64-1 (Acetone); 78-95-5 (chloroacetone)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19811119

Record Date Completed: 19811119

3/9/19

DIALOG(R)File 155:MEDLINE(R)

05204041 PMID: 118234

Molecular basis of altered enzyme specificities in a family of mutant amidases from Pseudomonas aeruginosa.

Paterson A; Clarke P H

Journal of general microbiology (ENGLAND) Sep 1979, 114 (1) p75-85, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A family of mutant amidases has been derived by experimental evolution of the **aliphatic amidase** of Pseudomonas aeruginosa strain PAC1. Mutation amiE16, in the structural gene for the enzyme, results in the production of the mutant B amidase by strain B6. This strain, unlike the wild-type, can utilize butyramide for growth. Strain B6 gave rise by a single mutational event to strain V9, utilizing valeramide, and strain PhB3, utilizing phenylacetamide. Strain V9 was not itself able to utilize phenylacetamide but gave rise by mutation to the phenylacetamide-utilizing mutant PhV1. Peptide 108 was isolated from chymotryptic digests of mutant amidases from strains B6, PhB3 and PhV1, but could not be detected in chymotryptic digests of the wild-type amidase. The sequence of peptide 108 was

established as Met-Arg-His-Gly-Asp-Ile-Phe. Thermolytic digests of mutant amidases from strains B6, PhB3, PhV1 and V9 were compared with digests of the wild-type amidase. A peptide of the composition Met, Arg, His, Gly2, Asp3, Ile, Ser3, Thr, Val was found in the digest of the wild-type amidase and was replaced in the digests of the mutant amidases by a peptide of the composition Met, Arg, His, Gly2, Asp3, Ile, Ser3, Thr, Val, Phe. Mutation amiE16 is common to the four mutant enzymes and can be accounted for by the mutation Ser leads to Phe. The sequence of the chymotryptic peptide corresponds with the N-terminal sequence of the amidase protein, and can also be related to the thermolysin peptides. It is concluded that mutation amiE16 is a Ser leads to Phe change at position 7 from the N-terminus and the effect of this on the enzyme conformation is discussed.

Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa --enzymology--EN; Amidohydrolases--genetics--GE; Amino Acid Sequence; Chromatography, Gel; Chymotrypsin; Genes, Structural; Mutation; Peptide Fragments--analysis--AN; Pseudomonas aeruginosa--genetics--GE; Substrate Specificity; Thermolysin

CAS Registry No.: 0 (Peptide Fragments)

Enzyme No.: EC 3.4.21.1 (Chymotrypsin); EC 3.4.24.27 (Thermolysin); EC 3.5. (Amidohydrolases)

Record Date Created: 19800317

Record Date Completed: 19800317

3/9/20

DIALOG(R)File 155:MEDLINE(R)

05202551 PMID: 533765

Local anesthetics block induction of the Pseudomonas alk regulon.

Benson S A

Journal of bacteriology (UNITED STATES) Dec 1979, 140 (3) p1123-5, ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The local anesthetics procaine and piperocaine blocked induction of the plasmid-determined enzymatic activities involved in the metabolism of n-alkanes in Pseudomonas putida. Procaine reversibly inhibited existing alkane hydroxylase activity. Induction of a soluble **aliphatic amidase** activity was not affected. These results support the hypothesis that induction of the plasmid-determined alkane metabolic system in P. putida involves a membrane component(s).

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Anesthetics, Local--pharmacology--PD; *Benzoates --pharmacology--PD; *Mixed Function Oxygenases--biosynthesis--BI; *Piperidines--pharmacology--PD; *Procaine--pharmacology--PD; *Pseudomonas --drug effects--DE; Alkanes--metabolism--ME; Amidohydrolases--biosynthesis --BI; Enzyme Induction--drug effects--DE; Mixed Function Oxygenases --genetics--GE; Plasmids; Pseudomonas--genetics--GE; Pseudomonas --metabolism--ME

CAS Registry No.: 0 (Alkanes); 0 (Anesthetics, Local); 0 (Benzoates); 0 (Piperidines); 0 (Plasmids); 59-46-1 (Procaine)

Enzyme No.: EC 1.- (Mixed Function Oxygenases); EC 3.5. (Amidohydrolases)

Record Date Created: 19800327

Record Date Completed: 19800327

3/9/21

DIALOG(R)File 155:MEDLINE(R)

05155937 PMID: 115712

A competition time-course method for following enzymic reactions applied to the hydrolysis of acetamide catalysed by an aliphatic amidase **.**

Hollaway M R; Ticho T

FEBS letters (NETHERLANDS) Oct 1 1979, 106 (1) p185-8, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Descriptors: *Amidohydrolases--metabolism--ME; Acetamides; Binding, Competitive; Hydrolysis; Kinetics; Mathematics; Pseudomonas aeruginosa --enzymology--EN; Time Factors
CAS Registry No.: 0 (Acetamides)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19800124
Record Date Completed: 19800124

3/9/22
DIALOG(R)File 155:MEDLINE(R)

05067535 PMID: 110589
Inhibition of the aliphatic amidase **from Pseudomonas aeruginosa by urea and related compounds.**
Gregoriou M; Brown P R
European journal of biochemistry / FEBS (GERMANY, WEST) May 2 1979, 96 (1) p101-8, ISSN 0014-2956 Journal Code: 0107600
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The time-dependent inhibition of amidase from Pseudomonas aeruginosa strain AI 3 by urea, hydroxyurea and cyanate displayed saturation kinetics fitting a model for the reaction sequence in which formation of a complex in a reversible step was followed by an irreversible step. Altered amidases from mutant strains AIU 1N and OUCH 4, selected for their resistance to inhibition of growth by urea and hydroxyurea respectively, had altered kinetic constants for inhibition indicating reduced binding capacity for the inhibitors. The substrate acetamide protected AI 3 amidase against inhibition by urea,.and altered Ki values for inhibition of the mutant amidases were paralleled by alterations in Km values for acetamide indicating that urea acted at the active site. Inhibition of AI 3 amidase involved the binding of one molecule of urea per molecule of enzyme. Urea inhibited amidase slowly regained activity at pH 7.2 through release of urea.
Descriptors: *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; *Urea--pharmacology--PD; Cyanates --pharmacology--PD; Enzyme Activation; Hydroxyurea--pharmacology--PD; Kinetics; Molecular Weight
CAS Registry No.: 0 (Cyanates); 127-07-1 (Hydroxyurea); 57-13-6 (Urea)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19790925
Record Date Completed: 19790925

3/9/23
DIALOG(R)File 155:MEDLINE(R)

05063754 PMID: 110350
Kinetic mechanism of the aliphatic amidase **from Pseudomonas aeruginosa.**
Woods M J; Findlater J D; Orsi B A
Biochimica et biophysica acta (NETHERLANDS) Mar 16 1979, 567 (1) p225-37, ISSN 0006-3002 Journal Code: 0217513
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM

Record type: Completed
Subfile: INDEX MEDICUS

The kinetic constants for hydrolysis and transfer (with hydroxylamine as the alternate acceptor) of the **aliphatic amidase** (acylamide amidohydrolase, EC 3.5.1.4) from Pseudomonas aeruginosa were determined for a variety of acetyl and propionyl derivatives. The results obtained were consistent with a ping-pong or substitution mechanism. Product inhibition, which was pH dependent, implicated an acyl-enzyme compound as a compulsory intermediate and indicated that ammonia combined additionally with the free enzyme in a dead-end manner. The uncompetitive activation of acetamide hydrolysis by hydroxylamine and the observation that the partitioning of products between acetic acid and acetohydroxamate was linearly dependent on the hydroxylamine concentration substantiated these conclusions and indicated that deacylation was at least partially rate limiting. With propionamide as the acyl donor apparently anomalous results, which included inequalities in certain kinetic constants and a hyperbolic dependence of the partition ratio on the hydroxylamine concentration, could be explained by postulating a compulsory isomerisation of the acyl-enzyme intermediate prior to the transfer reaction.

Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa --enzymology--EN; Acetamides; Acetic Acids--pharmacology--PD; Acylation; Amides; Amidohydrolases--antagonists and inhibitors--AI; Binding Sites; Hydrolysis; Hydroxylamines--pharmacology--PD; Kinetics; Models, Chemical; Propionates

CAS Registry No.: 0 (Acetamides); 0 (Acetic Acids); 0 (Amides); 0 (Hydroxylamines); 0 (Propionates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19790925

Record Date Completed: 19790925

3/9/24

DIALOG(R)File 155:MEDLINE(R)

04476995 PMID: 14704

Relationship between culture density and catabolite repression of an inducible aliphatic amidase **in a thermophilic bacillus.**

Thalenfeld B; Epstein I; Grossowicz N

Biochimica et biophysica acta (NETHERLANDS) Mar 29 1977, 497 (1) p112-21, ISSN 0006-3002 Journal Code: 0217513

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A direct correlation between the absorbance of a thermophilic bacillus and specific amidase activity was observed, which was found to depend on the cell density of the culture rather than on the time of contact of the culture with the inducer. Dilution of high density cultures caused the specific amidase activity to decrease. Environmental factors such as pH, concentration of inducer or degree of aeration, and level of NH+4 and glutamate had no effect on amidase synthesis. The decrease in amidase activity upon dilution could not be ascribed to destruction by oxygen or by inactivation or decay. Several lines of evidence suggest that catabolite repression is responsible for the phenomenon described. Succinate-grown cultures gave a stronger dilution effect thatn glutamate-grown cells. The mutant strain E-21, relatively resistant to catabolite repression, did not show the characteristic dilution effect nor the direct correlation between absorbance and specific amidase activity.

Descriptors: *Acetamides--pharmacology--PD; *Amidohydrolases--metabolism --ME; *Bacteria--enzymology--EN; Amidohydrolases--biosynthesis--BI; Ammonium Compounds--pharmacology--PD; Bacteria--growth and development--GD; Culture Media; Densitometry; Enzyme Induction; Enzyme Repression; Glutamates--pharmacology--PD; Hydrogen-Ion Concentration; Mutation; Osmolar Concentration

CAS Registry No.: 0 (Acetamides); 0 (Ammonium Compounds); 0 (Culture Media); 0 (Glutamates)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19770527
Record Date Completed: 19770527

3/9/25
DIALOG(R)File 155:MEDLINE(R)

04287097 PMID: 932686
Regulatory properties of an inducible aliphatic amidase **in a thermophilic bacillus.**
Thalenfeld B; Grossowicz N
Journal of general microbiology (ENGLAND) May 1976, 94 (1) p131-41, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A thermophilic bacillus growing on acetamide as both carbon and nitrogen sources produces an inducible amidase. This amidase hydrolysed the following amides in decreasing order or activity, in comparison with acetamide (1.00): propionamide (0.97), fluoroacetamide (0.84), formamide (0.35) and glycinamide (0.12). Cyanoacetamide, dimethylacetamide, dimethylformamide and urea also induced the synthesis of the amidase, but were not substrates of the enzyme. Studies with protoplasts suggest that the amidase is located in the cytoplasm. Glucose strongly inhibited amidase synthesis; and limiting nitrogen did not release this inhibition. Urea strongly inhibited amidase activity in a competitive manner; but the inhibition caused by iodoacetamide and cyanoacetamide was non-competitive. Both thioacetamide and thiourea were effective inhibitors of enzyme induction. Bacteria grown on a succinate-minimal medium exhibited a lag in amidase synthesis, which could be eliminated by decreasing the concentration of succinate. Acetate- or pyruvate-grown cultures behaved similarly, while those grown on alanine or glutamate exhibited no lag in enzyme induction. In the mutant strain E21, repression of amidase synthesis by glucose was much less evident and no lag for induction was apparent with any of the other carbon sources mentioned.
Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacillus--enzymology --EN; Acetamides--metabolism--ME; Amides--metabolism--ME; Amidohydrolases --metabolism--ME; Bacillus--growth and development--GD; Bacillus --metabolism--ME; Cell-Free System; Cytoplasm--enzymology--EN; Enzyme Induction--drug effects--DE; Enzyme Repression; Glucose--pharmacology--PD; Heat; Kinetics; Protoplasts--enzymology--EN; Thioacetamide--pharmacology --PD; Thiourea--pharmacology--PD; Urea--pharmacology--PD
CAS Registry No.: 0 (Acetamides); 0 (Amides); 50-99-7 (Glucose); 57-13-6 (Urea); 62-55-5 (Thioacetamide); 62-56-6 (Thiourea)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19760823
Record Date Completed: 19760823

3/9/26
DIALOG(R)File 155:MEDLINE(R)

04106765 PMID: 170365
Catabolite repression of Pseudomonas aeruginosa amidase: the effect of carbon source on amidase synthesis.
Smyth P F; Clarke P H
Journal of general microbiology (ENGLAND) Sep 1975, 90 (1) p81-90, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Synthesis of the Pseudomonas aeruginosa **aliphatic amidase** was repressed severely by succinate and malate and less severely by glucose,

acetate or lactate. Amidase synthesis in inducible and constitutive strains was stimulated by cyclic AMP, which also gave partial relief to catabolite repression produced by the addition of lactate to cultures growing in pyruvate medium. Mutants which were resistant to catabolite repression were isolated from succinate+lactamide medium.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas aeruginosa --enzymology--EN; Acetamides--pharmacology--PD; Acetates--pharmacology--PD; Citrates--pharmacology--PD; Cyclic AMP--pharmacology--PD; Enzyme Repression ; Glucose--pharmacology--PD; Glycerol--pharmacology--PD; Lactates --pharmacology--PD; Malates--pharmacology--PD; Mutation; Pseudomonas aeruginosa--metabolism--ME; Pyruvates--metabolism--ME; Succinates--pharmaco logy--PD

CAS Registry No.: 0 (Acetamides); 0 (Acetates); 0 (Citrates); 0 (Lactates); 0 (Malates); 0 (Pyruvates); 0 (Succinates); 50-99-7 (Glucose); 56-81-5 (Glycerol); 60-92-4 (Cyclic AMP)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19751220

Record Date Completed: 19751220

3/9/27

DIALOG(R)File 155:MEDLINE(R)

03660624 PMID: 4201665

Transition-state analogs of an aliphatic amidase **.**

Findlater J D; Orsi B A

FEBS letters (NETHERLANDS) Sep 1 1973, 35 (1) p109-11, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Pseudomonas aeruginosa--enzymology--EN; Acetates; Aldehydes ; Amidohydrolases--antagonists and inhibitors--AI; Ammonia; Catalysis; Ethanol; Ethylamines; Hydroxamic Acids; Kinetics

CAS Registry No.: 0 (Acetates); 0 (Aldehydes); 0 (Ethylamines); 0 (Hydroxamic Acids); 64-17-5 (Ethanol); 7664-41-7 (Ammonia)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19740115

Record Date Completed: 19740115

3/9/28

DIALOG(R)File 155:MEDLINE(R)

03551524 PMID: 4633800

The subunit structure of the aliphatic amidase **from Pseudomonas aeruginosa.**

Brown P R; Smyth M J; Clarke P H; Rosemeyer M A

European journal of biochemistry / FEBS (GERMANY, WEST) Apr 2 1973, 34 (1) p177-87, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--analysis--AN; *Pseudomonas aeruginosa --enzymology--EN; Acetamides; Alanine--analysis--AN; Amino Acids--analysis --AN; Chloromercuribenzoates; Chromatography, Gel; Cyanogen Bromide; Dicarboxylic Acids; Electrophoresis, Disc; Electrophoresis, Polyacrylamide Gel; Hydrogen-Ion Concentration; Imides; Indicators and Reagents; Macromolecular Systems; Methionine--analysis--AN; Molecular Weight; Osmolar Concentration; Peptides--analysis--AN; Protein Denaturation; Sodium Dodecyl Sulfate; Ultracentrifugation

CAS Registry No.: 0 (Acetamides); 0 (Amino Acids); 0 (Chloromercuribenzoates); 0 (Dicarboxylic Acids); 0 (Imides); 0

(Indicators and Reagents); 0 (Macromolecular Systems); 0 (Peptides); 151-21-3 (Sodium Dodecyl Sulfate); 506-68-3 (Cyanogen Bromide); 56-41-7 (Alanine); 63-68-3 (Methionine)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19730629
Record Date Completed: 19730629

3/9/29
DIALOG(R)File 155:MEDLINE(R)
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03398192 PMID: 4625925
Biochemical and immunological comparison of aliphatic amidases **produced by Pseudomonas species.**
Clarke P H
Journal of general microbiology (ENGLAND) Jul 1972, 71 (2) p241-57, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas--enzymology --EN; Acetamides--metabolism--ME; Antigens; Cell-Free System; Cross Reactions; Culture Media; Electrophoresis, Starch Gel; Enzyme Induction; Formamides--metabolism--ME; Genes, Regulator; Genes, Structural; Hydrolases --analysis--AN; Hydrolysis; Immune Sera; Immunodiffusion; Mutation; Phenotype; Pseudomonas--metabolism--ME; Pseudomonas aeruginosa--enzymology --EN; Pseudomonas aeruginosa--immunology--IM; Transferases--analysis--AN
CAS Registry No.: 0 (Acetamides); 0 (Antigens); 0 (Culture Media); 0 (Formamides); 0 (Immune Sera)
Enzyme No.: EC 2. (Transferases); EC 3. (Hydrolases); EC 3.5. (Amidohydrolases)
Record Date Created: 19720922
Record Date Completed: 19720922

3/9/30
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

02753312 PMID: 5821403
The isolation of an aliphatic amidase **from Pseudomonas aeruginosa.**
Lilly M D; Clarke P H; Houldsworth M; Currier J A; Dunnill P
Biotechnology and bioengineering (UNITED STATES) May 1969, 11 (3) p283-92, ISSN 0006-3592 Journal Code: 7502021
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Descriptors: *Aminohydrolases--isolation and purification--IP; *Pseudomonas--enzymology--EN; Chromatography, Ion Exchange; Methods; Precipitation; Technology
Enzyme No.: EC 3.5.4. (Aminohydrolases)
Record Date Created: 19691105
Record Date Completed: 19691105
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File 411:DIALINDEX(R)

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DIALINDEX(R)
   (c) 2004 The Dialog Corporation plc

*** DIALINDEX search results display in an abbreviated ***
*** format unless you enter the SET DETAIL ON command. ***
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   (To see banners, use SHOW FILES command)
?s aliphatic?/ti and amidase?/ti

Your SELECT statement is:
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              1    50: CAB Abstracts_1972-2004/Mar
              1    51: Food Sci.&Tech.Abs_1969-2004/Apr W2
              1    65: Inside Conferences_1993-2004/Apr W1
              6    71: ELSEVIER BIOBASE_1994-2004/Apr W1
             16    73: EMBASE_1974-2004/Apr W1
              2    98: General Sci Abs/Full-Text_1984-2004/Apr
       Examined  50 files
              2   143: Biol. & Agric. Index_1983-2004/Mar
             13   144: Pascal_1973-2004/Apr W1
             20   155: MEDLINE(R)_1966-2004/Apr W1
              2   156: ToxFile_1965-2004/Apr W2
              1   162: Global Health_1983-2004/Mar
              1   203: AGRIS_1974-2004/Feb
       Examined 100 files
              1   292: GEOBASE(TM)_1980-2004/Apr B1
              3   340: CLAIMS(R)/US Patent_1950-04/Apr 08
              1   342: Derwent Patents Citation Indx_1978-04/200420
              1   345: Inpadoc/Fam.& Legal Stat_1968-2003/UD=200414
       Examined 150 files
              1   348: EUROPEAN PATENTS_1978-2004/Apr W01
              1   349: PCT FULLTEXT_1979-2002/UB=20040408,UT=20040401
              4   357: Derwent Biotech Res.__1982-2004/Apr W2
>>>Term "TI" is not defined in file 390 and is ignored
             11   390: Beilstein Online_
>>>Term "TI" is not defined in file 398 and is ignored
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             25   399: CA SEARCH(R)_1967-2004/UD=14016
             12   434: SciSearch(R) Cited Ref Sci_1974-1989/Dec
             21   440: Current Contents Search(R)_1990-2004/Apr 13
       Examined 200 files
              3   654: US Pat.Full._1976-2004/Apr 06
       Examined 250 files

   27 files have one or more items; file list includes 283 files.
   One or more terms were invalid in 94 files.

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Temp SearchSave "TD803" stored
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Your last SELECT statement was:
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N3           21   440: Current Contents Search(R)_1990-2004/Apr 13
N4           20   155: MEDLINE(R)_1966-2004/Apr W1
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N8             12   434: SciSearch(R) Cited Ref Sci_1974-1989/Dec
N9             11*  390: Beilstein Online_
N10            10    34: SciSearch(R) Cited Ref Sci_1990-2004/Apr W1
   27 files have one or more items; file list includes 283 files.
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Ref         Items   File
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N12             4   357: Derwent Biotech Res.__1982-2004/Apr W2
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N14             3   654: US Pat.Full._1976-2004/Apr 06
N15             2    98: General Sci Abs/Full-Text_1984-2004/Apr
N16             2   143: Biol. & Agric. Index_1983-2004/Mar
N17             2   156: ToxFile_1965-2004/Apr W2
N18             1    50: CAB Abstracts_1972-2004/Mar
N19             1    51: Food Sci.&Tech.Abs_1969-2004/Apr W2
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N24             1   342: Derwent Patents Citation Indx_1978-04/200420
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N26             1   348: EUROPEAN PATENTS_1978-2004/Apr W01
N27             1   349: PCT FULLTEXT_1979-2002/UB=20040408,UT=20040401
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     $0.75  TELNET
     $4.72  Estimated cost this search
    $15.41  Estimated total session cost   2.900 DialUnits


SYSTEM:OS  - DIALOG OneSearch
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*File 399: Use is subject to the terms of your user/customer agreement.
Alert feature enhanced for multiple files, etc. See HELP ALERT.
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 to processing issues.
  File 654:US Pat.Full.  1976-2004/Apr 06
         (c) Format only 2004 The Dialog Corp.
*File 654: US published applications now online.  See HELP NEWS 654
for details.  Reassignments current through December 2, 2003.
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           5968  AMIDASE?/TI
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2/6/1 (Item 1 from file: 155)
13675690 PMID: 9364923
Identification and characterization of an aliphatic amidase **in Helicobacter pylori.**
Sep 1997

2/6/2 (Item 2 from file: 155)
12684768 PMID: 7607322
Pseudomonas aeruginosa aliphatic amidase **is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.**
Jul 3 1995

2/6/3 (Item 3 from file: 155)
12503813 PMID: 14500481
Presence of active aliphatic amidases **in Helicobacter species able to colonize the stomach.**
Oct 2003

2/6/4 (Item 4 from file: 155)
11451002 PMID: 11556902
Aliphatic **and enantioselective** amidases **: from hydrolysis to acyl transfer activity.**
Sep 2001

2/6/5 (Item 5 from file: 155)
11281780 PMID: 11359566
The AmiE aliphatic amidase **and AmiF formamidase of Helicobacter pylori: natural evolution of two enzyme paralogues.**
May 2001

2/6/6 (Item 6 from file: 155)
10616641 PMID: 10720437
Amino acid homologies between human biotinidase and bacterial aliphatic amidases **: putative identification of the active site of biotinidase.**
Feb 2000

2/6/7 (Item 7 from file: 155)
08977358 PMID: 1907262
Cloning and DNA sequence of amiC, a new gene regulating expression of the Pseudomonas aeruginosa aliphatic amidase **, and purification of the amiC product.**
Aug 1991

2/6/8 (Item 8 from file: 155)
08102032 PMID: 2495988
Nucleotide sequence of the aliphatic amidase **regulator gene (amiR) of Pseudomonas aeruginosa.**
Mar 27 1989

2/6/9 (Item 9 from file: 155)
07448694 PMID: 3108029
The amino acid sequence of the aliphatic amidase **from Pseudomonas aeruginosa.**

May 11 1987

2/6/10 (Item 10 from file: 155)
06715270 PMID: 6440948
Complementation analysis of the aliphatic amidase **genes of Pseudomonas aeruginosa.**
Dec 1984

2/6/11 (Item 11 from file: 155)
05674138 PMID: 6793036
Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase **from Pseudomonas aeruginosa.**
Dec 1 1980

2/6/12 (Item 12 from file: 155)
05155937 PMID: 115712
A competition time-course method for following enzymic reactions applied to the hydrolysis of acetamide catalysed by an aliphatic amidase **.**
Oct 1 1979

2/6/13 (Item 13 from file: 155)
05067535 PMID: 110589
Inhibition of the aliphatic amidase **from Pseudomonas aeruginosa by urea and related compounds.**
May 2 1979

2/6/14 (Item 14 from file: 155)
05063754 PMID: 110350
Kinetic mechanism of the aliphatic amidase **from Pseudomonas aeruginosa.**
Mar 16 1979

2/6/15 (Item 15 from file: 155)
04476995 PMID: 14704
Relationship between culture density and catabolite repression of an inducible aliphatic amidase **in a thermophilic bacillus.**
Mar 29 1977

2/6/16 (Item 16 from file: 155)
04287097 PMID: 932686
Regulatory properties of an inducible aliphatic amidase **in a thermophilic bacillus.**
May 1976

2/6/17 (Item 17 from file: 155)
03660624 PMID: 4201665
Transition-state analogs of an aliphatic amidase **.**
Sep 1 1973

2/6/18 (Item 18 from file: 155)
03551524 PMID: 4633800
The subunit structure of the aliphatic amidase **from Pseudomonas aeruginosa.**
Apr 2 1973

2/6/19 (Item 19 from file: 155)
03398192 PMID: 4625925
Biochemical and immunological comparison of aliphatic amidases **produced by Pseudomonas species.**

Jul 1972

2/6/20 (Item 20 from file: 155)
02753312 PMID: 5821403
The isolation of an aliphatic amidase **from Pseudomonas aeruginosa.**
May 1969

2/6/21 (Item 1 from file: 5)
0013215382 BIOSIS NO.: 200100387221
Helicobacter aliphatic amidase **AmiE polypeptides, and DNA sequences encoding those polypeptides**
2001

2/6/22 (Item 2 from file: 5)
0011231256 BIOSIS NO.: 199800025503
The aliphatic amidase **: Another way to produce ammonia in H. pylori?**
1997

2/6/23 (Item 3 from file: 5)
0003552704 BIOSIS NO.: 198273056631
UTILIZATION OF ALIPHATIC **AMIDES AND FORMATION OF 2 DIFFERENT** AMIDASES **BY ALCALIGENES-EUTROPHUS**
1981

2/6/24 (Item 4 from file: 5)
0003243180 BIOSIS NO.: 198171062139
CHLORO ACETONE AS AN ACTIVE SITE DIRECTED INHIBITOR OF THE ALIPHATIC AMIDASE **EC-3.5.1.4 FROM PSEUDOMONAS-AERUGINOSA**
1980

2/6/25 (Item 5 from file: 5)
0002800018 BIOSIS NO.: 198018039009
A COMPETITION TIME COURSE METHOD FOR FOLLOWING ENZYMIC REACTIONS APPLIED TO THE HYDROLYSIS OF ACETAMIDE CATALYZED BY AN ALIPHATIC AMIDASE **EC-3.5.1.4**
1979

2/6/26 (Item 6 from file: 5)
0002713001 BIOSIS NO.: 197968024500
KINETIC MECHANISM OF THE ALIPHATIC AMIDASE **EC-3.5.1.4 FROM PSEUDOMONAS-AERUGINOSA**
1979

2/6/27 (Item 7 from file: 5)
0002512657 BIOSIS NO.: 197916021652
PROPERTIES OF AN INDUCIBLE ALIPHATIC AMIDASE **FROM A THERMOPHILIC BACILLUS**
1978

2/6/28 (Item 8 from file: 5)
0001773358 BIOSIS NO.: 197612039497
SELECTIVE INHIBITION AND THE KINETIC MECHANISM OF THE ALIPHATIC AMIDASE **EC-3.5.1.4 OF PSEUDOMONAS-AERUGINOSA**
1974

2/6/29 (Item 9 from file: 5)
0001240272 BIOSIS NO.: 197356056714
THE SUBUNIT STRUCTURE OF THE ALIPHATIC AMIDASE **EC-3.5.1.4 FROM PSEUDOMONAS-AERUGINOSA**

1973

2/6/30 (Item 10 from file: 5)
0001123871 BIOSIS NO.: 197355010341
BIOCHEMICAL AND IMMUNOLOGICAL COMPARISON OF ALIPHATIC AMIDASES **PRODUCED BY PSEUDOMONAS-SPP**
1972

2/6/31 (Item 11 from file: 5)
0000445043 BIOSIS NO.: 197051041589
FORM AMIDASE **IN GUINEA-PIG LIVER PART 2 EFFECT OF** ALIPHATIC **ALCOHOLS**
1969

2/6/32 (Item 12 from file: 5)
0000398848 BIOSIS NO.: 197006085394
THE ALIPHATIC AMIDASES **OF PSEUDOMONAS-AERUGINOSA**
BOOK TITLE: ROSE, A. H. AND J. F. WILKINSON (EDITED BY). ADVANCES IN MICROBIAL PHYSIOLOGY, VOL. 4. XI + 353P. ILLUS. ACADEMIC PRESS INC., LTD.: LONDON, ENGLAND; NEW YORK, N.Y., U.S.A
1970

2/6/33 (Item 1 from file: 399)
DIALOG(R)File 399:(c) 2004 American Chemical Society. All rts. reserv.

Selective inhibition and the kinetic mechanism of the aliphatic amidase of Pseudomonase aeruginosa

2/6/34 (Item 1 from file: 144)
03352281 PASCAL No.: 81-0392478
CHLOROACETONE AS AN ACTIVE -RITE-DIRECTED INHIBITOR OF THE ALIPHATIC AMIDASE **FROM PSEUDOMONAS AERUGINOSA**
1980

2/6/35 (Item 1 from file: 357)
0312191 DBR Accession No.: 2003-13331
Purification, cloning, sequencing and over-expression in Escherichia coli of a regioselective aliphatic **nitrilase from Acidovorax facilis 72W - Acidovorax facilis stereospecific nitrile-hydratase and nitrile-**amidase **isolation involving vector plasmid pET-mediated nitrilase gene transfer and expression in Escherichia coli** 2003

2/6/36 (Item 2 from file: 357)
0230013 DBR Accession No.: 99-00114
New Helicobacter sp. aliphatic amidase **AmiE polypeptides and their encoding sequence - Helicobacter pylori recombinant protein preparation, vector expression in host cell and DNA probe and monoclonal antibody, used for infection diagnosis, recombinant vaccine or therapy** 1998

2/6/37 (Item 3 from file: 357)
0203740 DBR Accession No.: 96-14511
Utilization of acetonitrile and other aliphatic **nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and** amidase **activity** 1996

2/6/38 (Item 4 from file: 357)
0001358 DBR Accession No.: 82-00358
Aliphatic **nitrile hydratase from Arthrobacter sp.J-1 purification and characterization - and** amidase **production; catalysis of acetonitrile hydrolysis to form acetamide** 1982

2/6/39 (Item 1 from file: 340)
3528971
C/HELICOBACTER ALIPHATIC AMIDASE AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES; SCREENING BY CONTACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES

2/6/40 (Item 2 from file: 340)
3168988
C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITILES; ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION

2/6/41 (Item 3 from file: 340)
3096789
C/PREPARATION OF LACTAMS FROM ALIPHATIC ALPHA, OMEGA-DINITRILES; CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING ALIPHATIC NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND AMIDASE ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM

2/6/42 (Item 1 from file: 654)
4525521 **IMAGE Available
Derwent Accession: 1998-557106
Utility
C/ Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences encoding those polypeptides
; SCREENING BY CON TACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES

Fulltext Word Count: 5689
Number of Claims: 2
Exemplary or Independent Claim Number(s): 1
Number of Drawing Sheets: 23
Number of Figures: 12
Number of US cited patent references: 15
Number of non-US cited patent references: 15
Number of non-patent cited references: 26

2/6/43 (Item 2 from file: 654)
4166734
Derwent Accession: 1998-041747
Utility
C/ Preparation of lactams from aliphatic [alpha],[omega]-Dinitiles
; ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION

Fulltext Word Count: 19383
Number of Claims: 1
Exemplary or Independent Claim Number(s): 1
Number of US cited patent references: 4
Number of non-US cited patent references: 8
Number of non-patent cited references: 20

2/6/44 (Item 3 from file: 654)
4095232
Derwent Accession: 1998-041747
Utility
C/ Preparation of lactams from aliphatic [alpha],[omega]-dinitriles
; CONTACTIN G DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING

ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**

Fulltext Word Count: 20552
Number of Claims: 20
Exemplary or Independent Claim Number(s): 1
Number of US cited patent references: 5
Number of non-US cited patent references: 8
Number of non-patent cited references: 20

2/6/45 (Item 1 from file: 65)
03333046 INSIDE CONFERENCE ITEM ID: CN035225547
Identification of an aliphatic amidase **in H. pylori**
CONFERENCE: Campylobacter, heliobacter & related organisms-
International workshop; 9th (199709)

2/6/46 (Item 1 from file: 342)
03324989 WPI Acc No: 98-557106/47
New Helicobacter aliphatic amidase AmiE polypeptides and their encoding sequences...

2/6/47 (Item 1 from file: 348)
01000868
HELICOBACTER ALIPHATIC AMIDASE **POLYPEPTIDES, DNA SEQUENCES ENCODING THOSE POLYPEPTIDES AND USES THEREOF**
HELICOBACTER ALIPHATISCHE AMIDASE **POLYPEPTIDEN, DAFUR KODIERENDE DNA SEQUENZEN UND DEREN VERWENDUNGEN**
POLYPEPTIDES DE L' AMIDASE **ALIPHATIQUE AmiE D'$i(HELICOBACTER)ET SEQUENCES D'ADN CODANT LESDITS POLYPEPTIDES**
LANGUAGE (Publication,Procedural,Application): English; English; English

2/6/48 (Item 1 from file: 349)
00453630
i(HELICOBACTER) ALIPHATIC AMIDASE **POLYPEPTIDES, DNA SEQUENCES ENCODING THOSE POLYPEPTIDES AND USES THEREOF**
POLYPEPTIDES DE L' AMIDASE **ALIPHATIQUE AmiE D'i(HELICOBACTER)ET SEQUENCES D'ADN CODANT LESDITS POLYPEPTIDES**
Publication Language: English
Fulltext Availability:
Detailed Description
Claims
Fulltext Word Count: 9017
Publication Year: 1998
?logoff hold
13apr04 12:12:25 User228206 Session D2146.6
$0.44 0.138 DialUnits File155
$0.00 20 Type(s) in Format 6
$0.00 20 Types
$0.44 Estimated cost File155
$0.87 0.155 DialUnits File5
$0.00 12 Type(s) in Format 6
$0.00 12 Types
$0.87 Estimated cost File5
$0.96 0.076 DialUnits File399
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$1.51 Estimated cost File399
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$1.67 Estimated cost File440
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$0.00 1 Types
$0.16 Estimated cost File144
$0.53 0.027 DialUnits File357

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          $0.00   4 Types
     $0.53  Estimated cost File357
          $0.97     0.061 DialUnits File340
            $0.75   3 Type(s) in Format  6
          $0.75   3 Types
     $1.72  Estimated cost File340
          $0.84     0.143 DialUnits File654
            $0.75   3 Type(s) in Format  6
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     $1.59  Estimated cost File654
          $0.04     0.015 DialUnits File143
     $0.04  Estimated cost File143
          $0.11     0.020 DialUnits File156
     $0.11  Estimated cost File156
          $0.07     0.015 DialUnits File50
     $0.07  Estimated cost File50
          $0.05     0.012 DialUnits File65
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          $0.04     0.015 DialUnits File203
     $0.04  Estimated cost File203
          $0.24     0.015 DialUnits File342
            $0.00   1 Type(s) in Format  6
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          $0.26     0.057 DialUnits File348
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     $0.51  Estimated cost File348
          $0.22     0.047 DialUnits File349
            $0.25   1 Type(s) in Format  6
          $0.25   1 Types
     $0.47  Estimated cost File349
          OneSearch, 16 files,   0.919 DialUnits FileOS
     $0.24  TELNET
    $10.26  Estimated cost this search
    $25.67  Estimated total session cost    3.819 DialUnits


### Status: Signed Off. (4 minutes)

### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 31060000009999...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 04.02.00D

Reconnected in file OS 13apr04 12:19:02
*
*
* ALL NEW CURRENT YEAR RANGES HAVE BEEN * * *
* * * INSTALLED   * * *

SYSTEM:OS  - DIALOG OneSearch
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File 155:MEDLINE(R) 1966-2004/Apr W1
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File 357:Derwent Biotech Res. _1982-2004/Apr W2
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File 340:CLAIMS(R)/US Patent 1950-04/Apr 08
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*File 654: US published applications now online. See HELP NEWS 654
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(c) 2004 European Patent Office
File 349:PCT FULLTEXT 1979-2002/UB=20040408,UT=20040401
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Set	Items	Description

Cost is in DialUnits
?ds

Set	Items	Description
S1	127	ALIPHATIC?/TI AND AMIDASE?/TI
S2	48	RD (unique items)

?t s2/9/1 2 7 8 9 10 11 13 14 16 19 22 45

2/9/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

13675690 PMID: 9364923
Identification and characterization of an aliphatic amidase **in Helicobacter pylori.**
Skouloubris S; Labigne A; De Reuse H
Unite de Pathogenie Bacterienne des Muqueuses, Institut Pasteur, Paris, France.
Molecular microbiology (ENGLAND) Sep 1997, 25 (5) p989-98, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
We report, for the first time, the presence in Helicobacter pylori of an

aliphatic amidase that, like urease, contributes to ammonia production. Aliphatic amidases are cytoplasmic acylamide amidohydrolases (EC 3.5.1.4) hydrolysing short-chain aliphatic amides to produce ammonia and the corresponding organic acid. The finding of an aliphatic amidase in H. pylori was unexpected as this enzyme has only previously been described in bacteria of environmental (soil or water) origin. The H. pylori amidase gene amiE (1017 bp) was sequenced, and the deduced amino acid sequence of AmiE (37746Da) is very similar (75% identity) to the other two sequenced aliphatic amidases, one from Pseudomonas aeruginosa and one from Rhodococcus sp. R312. Amidase activity was measured as the release of ammonia by sonicated crude extracts from H. pylori strains and from recombinant Escherichia coli strains overproducing the H. pylori amidase. The substrate specificity was analysed with crude extracts from H. pylori cells grown in vitro; the best substrates were propionamide, acrylamide and acetamide. Polymerase chain reaction (PCR) amplification of an internal amiE sequence was obtained with each of 45 different H. pylori clinical isolates, suggesting that amidase is common to all H. pylori strains. A H. pylori mutant (N6-836) carrying an interrupted amiE gene was constructed by allelic exchange. No amidase activity could be detected in N6-836. In a N6-urease negative mutant, amidase activity was two- to threefold higher than in the parental strain N6. Crude extracts of strain N6 slowly hydrolysed formamide. This activity was affected in neither the amidase negative strain (N6-836) nor a double mutant strain deficient in both amidase and urease activities, suggesting the presence of an independent discrete formamidase in H. pylori. The existence of an aliphatic amidase, a correlation between the urease and amidase activities and the possible presence of a formamidase indicates that H. pylori has a large range of possibilities for intracellular ammonia production.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Amidohydrolases--analysis--AN; *Helicobacter pylori --enzymology--EN; Amino Acid Sequence; Cloning, Molecular; DNA, Recombinant ; Escherichia coli--enzymology--EN; Escherichia coli--genetics--GE; Genes, Structural, Bacterial--genetics--GE; Helicobacter pylori--chemistry--CH; Helicobacter pylori--genetics--GE; Molecular Sequence Data; Mutation --genetics--GE; Recombinant Proteins--genetics--GE; Recombinant Proteins --metabolism--ME; Sequence Homology, Amino Acid; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/Y12252

CAS Registry No.: 0 (DNA, Recombinant); 0 (Recombinant Proteins)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19980129

Record Date Completed: 19980129

2/9/2 (Item 2 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

12684768 PMID: 7607322

Pseudomonas aeruginosa aliphatic amidase **is related to the nitrilase/cyanide hydratase enzyme family and Cys166 is predicted to be the active site nucleophile of the catalytic mechanism.**

Novo C; Tata R; Clemente A; Brown P R

Instituto Nacional de Engenharia e Tecnologia Industrial/IBQTA, Queluz, Portugal.

FEBS letters (NETHERLANDS) Jul 3 1995, 367 (3) p275-9, ISSN 0014-5793 Journal Code: 0155157

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A database search indicated homology between some members of the nitrilase/cyanide hydratase family, Pseudomonas aeruginosa and Rhodococcus erythropolis amidases and several other proteins, some of unknown function. BLOCK and PROFILE searches confirmed these relationships and showed that four regions of the P. aeruginosa amidase had significant homology with corresponding regions of nitrilases. A phylogenetic tree placed the P. aeruginosa and R. erythropolis amidases in a group with nitrilases but separated other amidases into three groups. The active site cysteine in

nitrilases is conserved in the P. aeruginosa amidase indicating that Cys166 is the active site nucleophile.
Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--chemistry--CH; *Pseudomonas aeruginosa --enzymology--EN; Amidohydrolases--metabolism--ME; Amino Acid Sequence; Aminohydrolases--chemistry--CH; Binding Sites; Cysteine--chemistry--CH; Hydro-Lyases--chemistry--CH; Molecular Sequence Data; Phylogeny; Sequence Alignment; Sequence Homology, Amino Acid
CAS Registry No.: 52-90-4 (Cysteine)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase); EC 3.5.4. (Aminohydrolases); EC 3.5.5.1 (nitrilase); EC 4.2.1. (Hydro-Lyases); EC 4.2.1.66 (cyanide hydratase)
Record Date Created: 19950817
Record Date Completed: 19950817

2/9/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08977358 PMID: 1907262
Cloning and DNA sequence of amiC, a new gene regulating expression of the Pseudomonas aeruginosa aliphatic amidase **, and purification of the amiC product.**
Wilson S; Drew R
Department of Biochemistry, University College London, United Kingdom.
Journal of bacteriology (UNITED STATES) Aug 1991, 173 (16) p4914-21, ISSN 0021-9193 Journal Code: 2985120R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Using in vitro-constructed deletions and subcloned DNA fragments, we have identified a new gene, amiC, which regulates expression of the inducible Pseudomonas aeruginosa aliphatic amidase activity. The DNA sequence of the gene has been determined, and an open reading frame encoding a polypeptide of 385 amino acids (molecular mass, 42,834 Da) has been identified. A search of sequence libraries has failed to find homologies with other published sequences. The amiC translation termination codon (A)TGA overlaps the initiation codon for the downstream amiR transcription antitermination factor gene, implying that the amiCR operon is coordinately regulated. Disruption of the amiC open reading frame by insertion and deletion leads to constitutive amidase synthesis, suggesting that AmiC is a negative regulator. This is confirmed by the finding that a broad-host-range expression vector carrying amiC (pSW41) represses amidase expression in a series of previously characterized P. aeruginosa amidase-constitutive mutants. The AmiC polypeptide has been purified from PAC452(pSW41), and N-terminal amino acid sequencing has confirmed the gene identification.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: *Amidohydrolases--genetics--GE; *Bacterial Proteins --isolation and purification--IP; *Genes, Regulator--genetics--GE; *Periplasmic Binding Proteins; *Pseudomonas aeruginosa--genetics--GE; *Repressor Proteins--isolation and purification--IP; Amidohydrolases --biosynthesis--BI; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Base Sequence; Enzyme Induction; Escherichia coli--metabolism--ME; Gene Expression Regulation, Bacterial; Molecular Sequence Data; Mutation --genetics--GE; Plasmids--genetics--GE; Pseudomonas aeruginosa--enzymology --EN; Repressor Proteins--genetics--GE; Restriction Mapping
Molecular Sequence Databank No.: GENBANK/M43175; GENBANK/M74478; GENBANK/M74479; GENBANK/M74480; GENBANK/M74481; GENBANK/M74482; GENBANK/M74483; GENBANK/M74484; GENBANK/S45931; GENBANK/S45975; GENBANK/X13776
CAS Registry No.: 0 (Bacterial Proteins); 0 (Periplasmic Binding Proteins); 0 (Plasmids); 0 (Repressor Proteins); 142462-53-1 (AmiC protein, Pseudomonas aeruginosa)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19910905
Record Date Completed: 19910905

2/9/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08102032 PMID: 2495988
Nucleotide sequence of the aliphatic amidase **regulator gene (amiR) of Pseudomonas aeruginosa.**
Lowe N; Rice P M; Drew R E
Department of Biochemistry, University College London, England.
FEBS letters (NETHERLANDS) Mar 27 1989, 246 (1-2) p39-43, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The nucleotide sequence of a 1001 bp ClaI/XhoI DNA fragment encoding the amidase regulator gene (amiR) from Pseudomonas aeruginosa has been determined. The sequence derives from strain PAC433, a constitutive high expressing amidase mutant, and contains two overlapping open reading frames. Analysis of the sequence has identified one of the reading frames as amiR. The gene encodes a 196 amino acid polypeptide which shows a strong bias towards codons with G or C in the third position. The amiR gene shows no sequence homology with other bacterial regulator proteins.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Regulator; *Pseudomonas aeruginosa--genetics--GE; Amino Acid Sequence; Base Sequence; Codon; Deoxyribonucleases, Type II Site-Specific; Molecular Sequence Data; Molecular Weight; Pseudomonas aeruginosa--enzymology--EN; Translation, Genetic
Molecular Sequence Databank No.: GENBANK/X13776
CAS Registry No.: 0 (Codon)
Enzyme No.: EC 3.1.21.- (endodeoxyribonuclease ClaI); EC 3.1.21.- (endodeoxyribonuclease XhoI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific); EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)
Record Date Created: 19890608
Record Date Completed: 19890608

2/9/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07448694 PMID: 3108029
The amino acid sequence of the aliphatic amidase **from Pseudomonas aeruginosa.**
Ambler R P; Auffret A D; Clarke P H
FEBS letters (NETHERLANDS) May 11 1987, 215 (2) p285-90, ISSN 0014-5793 Journal Code: 0155157
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Amino acid sequence studies show that the aliphatic amidase (EC 3.5.1.4) from Pseudomonas aeruginosa PAC142 consists of a single polypeptide chain of 346 residues, giving an Mr of 38,400. The evidence from the amino acid studies is in complete agreement with that deduced from the DNA sequence of the amiE gene. Studies of the protein from Pseudomonas putida A87 show that it differs from the Ps. aeruginosa protein by about 30 amino acid substitutions. It now becomes possible to relate changes in the enzyme which result in altered specificity to structural changes in the protein.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--analysis--AN; *Pseudomonas aeruginosa --enzymology--EN; Amino Acid Sequence; Peptide Fragments--analysis--AN
CAS Registry No.: 0 (Peptide Fragments)
Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19870626
Record Date Completed: 19870626

2/9/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

06715270 PMID: 6440948
Complementation analysis of the aliphatic amidase **genes of Pseudomonas aeruginosa.**
Drew R
Journal of general microbiology (ENGLAND) Dec 1984, 130 (Pt 12) p3101-11, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A plasmid, pCL34, capable of autonomous replication in Escherichia coli and Pseudomonas aeruginosa has been constructed which carries the promoter and structural gene (amiE) for P. aeruginosa amidase, but not the regulator gene (amiR). Plasmid pCL34 has been mobilized from E. coli to P. aeruginosa using the broad host range plasmid RP4. Complementation studies were performed in P. aeruginosa strains carrying various amidase mutations. Measurements of amidase activity in the recipients under inducing, non-inducing and repressing conditions showed trans-complementation by the chromosomally located regulator gene product. These results confirmed the positive control model for amidase gene expression. Levels of amidase expression seen during these studies were approximately threefold higher than in the parental, amidase-positive strains.
Tags: Support, Non-U.S. Gov't
Descriptors: *Amidohydrolases--genetics--GE; *Genes, Bacterial; *Genes, Structural; *Pseudomonas aeruginosa--genetics--GE; Chromosome Mapping; Gene Expression Regulation; Genetic Complementation Test; Phenotype; Plasmids; Pseudomonas aeruginosa--enzymology--EN; Transformation, Bacterial
CAS Registry No.: 0 (Plasmids)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19850314
Record Date Completed: 19850314

2/9/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2004 The Dialog Corp. All rts. reserv.

05674138 PMID: 6793036
Chloroacetone as an active-site-directed inhibitor of the aliphatic amidase **from Pseudomonas aeruginosa.**
Hollaway M R; Clarke P H; Ticho T
Biochemical journal (ENGLAND) Dec 1 1980, 191 (3) p811-26, ISSN 0264-6021 Journal Code: 2984726R
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
1. Chloroacetone (I) was shown to be an active-site-directed inhibitor of the aliphatic amidase (EC 3.5.1.4) from Pseudomonas aeruginosa strain PAC142.2. This inhibitor reacted with the enzyme in two stages: the first involving the reversible formation of an enzymically inactive species, EI, and the second the formation of a species, EX, from which enzymic activity could not be recovered. 3. Different types of kinetic experiment were conducted to test conformity of the reaction to the scheme: E + I k+1 Equilibrium k-1 EI Leads to K+2 EX A computer-based analysis of the results was carried out and values of the individual rate constants were determined. 4. No direct evidence for a binding step before the formation of EI could be obtained, as with [E]0 Less Than [I]0 the observed first-order rate constant for the formation of EI was directly proportional

to the concentration of chloroacetone up to 1.2 mM (above this concentration the reaction became too rapid to follow even by the stopped-flow method developed to investigate fast inhibition). 5. The value of k+1 exhibited a bell-shaped pH-dependency with a maximum value of about 3 X 10(3) M-1. S-1 at pH6 and apparent pKa values of 7.8 and about 4.8.6. The values of k-1 and K+2 were similar and changed with the time of reaction from values of about 3 X 10(-3) S-1 (pH8.6) at short times to about one-sixth this value for longer periods of incubation. In this respect the simple reaction scheme is insufficient to describe the inhibition process. 7. The overall inhibition reaction is rapid, whether it is considered in relation to the expected chemical reactivity of chloroacetone, the rate of reaction of other enzymes with substrate analogues containing the chloromethyl group, or the rate of the amidase-catalysed hydrolysis of N-methylacetamide, a substrate that is nearly isosteric with chloroacetone. 8. Acetamide protected the amidase from inhibition by chloroacetone, and the concentration-dependence of the protection gave a value of an apparent dissociation constant similar to the Km value for this substrate. 9. Addition of acetamide to solutions of the species EI led to a slow recovery of activity. Recovery of active enzyme was also observed after dilution of a solution of EI in the absence of substrate. 10. The species EI is considered not to be a simple adsorption complex, and the possibilities are discussed that it may be a tetrahedral carbonyl adduct, a Schiff base (azomethine) or a complex in which the enzyme has undergone a structural change. The species EX is probably a derivative in which there is a covalent bond between a group in the enzyme and the C-1 atom of the inhibitor.

Descriptors: *Acetone--analogs and derivatives--AA; *Amidohydrolases --antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; Acetamides--pharmacology--PD; Acetone--pharmacology--PD; Binding Sites; Kinetics; Models, Chemical

CAS Registry No.: 0 (Acetamides); 67-64-1 (Acetone); 78-95-5 (chloroacetone)

Enzyme No.: EC 3.5. (Amidohydrolases); EC 3.5.1.4 (amidase)

Record Date Created: 19811119

Record Date Completed: 19811119

2/9/13 (Item 13 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

05067535 PMID: 110589

Inhibition of the aliphatic amidase **from Pseudomonas aeruginosa by urea and related compounds.**

Gregoriou M; Brown P R

European journal of biochemistry / FEBS (GERMANY, WEST) May 2 1979, 96 (1) p101-8, ISSN 0014-2956 Journal Code: 0107600

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The time-dependent inhibition of amidase from Pseudomonas aeruginosa strain AI 3 by urea, hydroxyurea and cyanate displayed saturation kinetics fitting a model for the reaction sequence in which formation of a complex in a reversible step was followed by an irreversible step. Altered amidases from mutant strains AIU 1N and OUCH 4, selected for their resistance to inhibition of growth by urea and hydroxyurea respectively, had altered kinetic constants for inhibition indicating reduced binding capacity for the inhibitors. The substrate acetamide protected AI 3 amidase against inhibition by urea,.and altered Ki values for inhibition of the mutant amidases were paralleled by alterations in Km values for acetamide indicating that urea acted at the active site. Inhibition of AI 3 amidase involved the binding of one molecule of urea per molecule of enzyme. Urea inhibited amidase slowly regained activity at pH 7.2 through release of urea.

Descriptors: *Amidohydrolases--antagonists and inhibitors--AI; *Pseudomonas aeruginosa--enzymology--EN; *Urea--pharmacology--PD; Cyanates --pharmacology--PD; Enzyme Activation; Hydroxyurea--pharmacology--PD;

Kinetics; Molecular Weight
CAS Registry No.: 0 (Cyanates); 127-07-1 (Hydroxyurea); 57-13-6 (Urea)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19790925
Record Date Completed: 19790925

2/9/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05063754 PMID: 110350
Kinetic mechanism of the aliphatic amidase **from Pseudomonas aeruginosa.**
Woods M J; Findlater J D; Orsi B A
Biochimica et biophysica acta (NETHERLANDS) Mar 16 1979, 567 (1) p225-37, ISSN 0006-3002 Journal Code: 0217513
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The kinetic constants for hydrolysis and transfer (with hydroxylamine as the alternate acceptor) of the aliphatic amidase (acylamide amidohydrolase, EC 3.5.1.4) from Pseudomonas aeruginosa were determined for a variety of acetyl and propionyl derivatives. The results obtained were consistent with a ping-pong or substitution mechanism. Product inhibition, which was pH dependent, implicated an acyl-enzyme compound as a compulsory intermediate and indicated that ammonia combined additionally with the free enzyme in a dead-end manner. The uncompetitive activation of acetamide hydrolysis by hydroxylamine and the observation that the partitioning of products between acetic acid and acetohydroxamate was linearly dependent on the hydroxylamine concentration substantiated these conclusions and indicated that deacylation was at least partially rate limiting. With propionamide as the acyl donor apparently anomalous results, which included inequalities in certain kinetic constants and a hyperbolic dependence of the partition ratio on the hydroxylamine concentration, could be explained by postulating a compulsory isomerisation of the acyl-enzyme intermediate prior to the transfer reaction.
Descriptors: *Amidohydrolases--metabolism--ME; *Pseudomonas aeruginosa --enzymology--EN; Acetamides; Acetic Acids--pharmacology--PD; Acylation; Amides; Amidohydrolases--antagonists and inhibitors--AI; Binding Sites; Hydrolysis; Hydroxylamines--pharmacology--PD; Kinetics; Models, Chemical; Propionates
CAS Registry No.: 0 (Acetamides); 0 (Acetic Acids); 0 (Amides); 0 (Hydroxylamines); 0 (Propionates)
Enzyme No.: EC 3.5. (Amidohydrolases)
Record Date Created: 19790925
Record Date Completed: 19790925

2/9/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04287097 PMID: 932686
Regulatory properties of an inducible aliphatic amidase **in a thermophilic bacillus.**
Thalenfeld B; Grossowicz N
Journal of general microbiology (ENGLAND) May 1976, 94 (1) p131-41, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
A thermophilic bacillus growing on acetamide as both carbon and nitrogen sources produces an inducible amidase. This amidase hydrolysed the

following amides in decreasing order or activity, in comparison with acetamide (1.00): propionamide (0.97), fluoroacetamide (0.84), formamide (0.35) and glycinamide (0.12). Cyanoacetamide, dimethylacetamide, dimethylformamide and urea also induced the synthesis of the amidase, but were not substrates of the enzyme. Studies with protoplasts suggest that the amidase is located in the cytoplasm. Glucose strongly inhibited amidase synthesis; and limiting nitrogen did not release this inhibition. Urea strongly inhibited amidase activity in a competitive manner; but the inhibition caused by iodoacetamide and cyanoacetamide was non-competitive. Both thioacetamide and thiourea were effective inhibitors of enzyme induction. Bacteria grown on a succinate-minimal medium exhibited a lag in amidase synthesis, which could be eliminated by decreasing the concentration of succinate. Acetate- or pyruvate-grown cultures behaved similarly, while those grown on alanine or glutamate exhibited no lag in enzyme induction. In the mutant strain E21, repression of amidase synthesis by glucose was much less evident and no lag for induction was apparent with any of the other carbon sources mentioned.

Descriptors: *Amidohydrolases--biosynthesis--BI; *Bacillus--enzymology --EN; Acetamides--metabolism--ME; Amides--metabolism--ME; Amidohydrolases --metabolism--ME; Bacillus--growth and development--GD; Bacillus --metabolism--ME; Cell-Free System; Cytoplasm--enzymology--EN; Enzyme Induction--drug effects--DE; Enzyme Repression; Glucose--pharmacology--PD; Heat; Kinetics; Protoplasts--enzymology--EN; Thioacetamide--pharmacology --PD; Thiourea--pharmacology--PD; Urea--pharmacology--PD

CAS Registry No.: 0 (Acetamides); 0 (Amides); 50-99-7 (Glucose); 57-13-6 (Urea); 62-55-5 (Thioacetamide); 62-56-6 (Thiourea)

Enzyme No.: EC 3.5. (Amidohydrolases)

Record Date Created: 19760823

Record Date Completed: 19760823

2/9/19 (Item 19 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

03398192 PMID: 4625925

Biochemical and immunological comparison of aliphatic amidases **produced by Pseudomonas species.**

Clarke P H

Journal of general microbiology (ENGLAND) Jul 1972, 71 (2) p241-57, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Descriptors: *Amidohydrolases--biosynthesis--BI; *Pseudomonas--enzymology --EN; Acetamides--metabolism--ME; Antigens; Cell-Free System; Cross Reactions; Culture Media; Electrophoresis, Starch Gel; Enzyme Induction; Formamides--metabolism--ME; Genes, Regulator; Genes, Structural; Hydrolases --analysis--AN; Hydrolysis; Immune Sera; Immunodiffusion; Mutation; Phenotype; Pseudomonas--metabolism--ME; Pseudomonas aeruginosa--enzymology --EN; Pseudomonas aeruginosa--immunology--IM; Transferases--analysis--AN

CAS Registry No.: 0 (Acetamides); 0 (Antigens); 0 (Culture Media); 0 (Formamides); 0 (Immune Sera)

Enzyme No.: EC 2. (Transferases); EC 3. (Hydrolases); EC 3.5. (Amidohydrolases)

Record Date Created: 19720922

Record Date Completed: 19720922

2/9/22 (Item 2 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

0011231256 BIOSIS NO.: 199800025503

The aliphatic amidase **: Another way to produce ammonia in H. pylori?**

AUTHOR: Skouloubris S; Labigne A; De Reuse H

AUTHOR ADDRESS: Inst. Pasteur, Paris, France**France

JOURNAL: Gut 41 (SUPPL. 1): pA14 1997 1997
MEDIUM: print
CONFERENCE/MEETING: European Helicobacter Pylori Study Group Xth International Workshop on Gastroduodenal Pathology and Helicobacter Pylori Lisbon, Portugal September 11-14, 1997; 19970911
SPONSOR: European Helicobacter pylori Study Group
ISSN: 0017-5749
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English
REGISTRY NUMBERS: 7664-41-7: ammonia
DESCRIPTORS:
MAJOR CONCEPTS: Enzymology--Biochemistry and Molecular Biophysics; Molecular Genetics--Biochemistry and Molecular Biophysics
BIOSYSTEMATIC NAMES: Aerobic Helical or Vibrioid Gram-Negatives--Eubacteria, Bacteria, Microorganisms
ORGANISMS: Helicobacter-pylori (Aerobic Helical or Vibrioid Gram-Negatives)
COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: aliphatic amidase; ammonia--metabolic production pathways
MISCELLANEOUS TERMS: Meeting Abstract; Meeting Abstract
CONCEPT CODES:
31500 Genetics of bacteria and viruses
10050 Biochemistry methods - General
10054 Biochemistry methods - Proteins, peptides and amino acids
10808 Enzymes - Physiological studies
13002 Metabolism - General metabolism and metabolic pathways
13012 Metabolism - Proteins, peptides and amino acids
31000 Physiology and biochemistry of bacteria
00520 General biology - Symposia, transactions and proceedings
10060 Biochemistry studies - General
10064 Biochemistry studies - Proteins, peptides and amino acids
36002 Medical and clinical microbiology - Bacteriology
BIOSYSTEMATIC CODES:
06210 Aerobic Helical or Vibrioid Gram-Negatives

2/9/45 (Item 1 from file: 65)
DIALOG(R)File 65:Inside Conferences

03333046 INSIDE CONFERENCE ITEM ID: CN035225547
Identification of an aliphatic amidase **in H. pylori**
de Reuse, H.; Skouloubris, S.; Labigne, A.
CONFERENCE: Campylobacter, heliobacter & related organisms-International workshop; 9th
P: 490
Institute of Child Health, 1998
ISBN: 0620216794
LANGUAGE: English DOCUMENT TYPE: Conference Papers
CONFERENCE EDITOR(S): Lastovica, A. J.; Newell, D. G.; Lastovica, E. E.
CONFERENCE SPONSOR: University of Cape Town
CONFERENCE LOCATION: Cape Town
CONFERENCE DATE: Sep 1997 (199709) (199709)

BRITISH LIBRARY ITEM LOCATION: m00/31914
DESCRIPTORS: campylobacter; heliobacter; organisms; child health
?t s2/3,kwic/36 37 39 40 41 43 44 48
>>>KWIC option is not available in file(s): 399

2/3,KWIC/36 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0230013 DBR Accession No.: 99-00114 PATENT
New Helicobacter sp. aliphatic amidase **AmiE polypeptides and their encoding sequence - Helicobacter pylori recombinant protein preparation, vector expression in host cell and DNA probe and**

monoclonal antibody, used for infection diagnosis, recombinant vaccine or therapy
AUTHOR: de Reuse H; Skouloubris S; Labigne A
CORPORATE SOURCE: Paris, France.
PATENT ASSIGNEE: Inst.Pasteur-Paris; INSERM 1998
PATENT NUMBER: WO 9844094 PATENT DATE: 981008 WPI ACCESSION NO.: 98-557106 (9847)
PRIORITY APPLIC. NO.: US 41745 APPLIC. DATE: 970328
NATIONAL APPLIC. NO.: WO 98EP1824 APPLIC. DATE: 980327
LANGUAGE: English

New Helicobacter sp. aliphatic amidase **AmiE polypeptides and their encoding sequence**

2/3,KWIC/37 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0203740 DBR Accession No.: 96-14511
Utilization of acetonitrile and other aliphatic **nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and** amidase **activity**
AUTHOR: Linardi V R; Dias J C T; Rosa C A
CORPORATE AFFILIATE: Univ.Minas-Gerais-Fed.Inst.Biol.Sci.
CORPORATE SOURCE: Departamento de Microbiologia, Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais, C.P. 486, Belo Horizonte, MG 31270-901, Brazil.
JOURNAL: FEMS Microbiol.Lett. (144, 1, 67-71) 1996
ISSN: 0378-1097 CODEN: FMLED7
LANGUAGE: English

Utilization of acetonitrile and other aliphatic **nitriles by a Candida famata strain - acetonitrile degradation using nitrile-hydratase and** amidase **activity**

2/3,KWIC/39 (Item 1 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

3528971 0122998
C/HELICOBACTER ALIPHATIC AMIDASE **AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES; SCREENING BY CONTACTING ENZYME WITH COMPOUND, AND SELECTING COMPOUND WHICH INHIBITS ENZYME ACTIVITY; ANTIULCER AGENTS; BACTERICIDES**
Inventors: De Reuse Hilde (FR); Labigne Agnes (FR); Skouloubris Stephane (FR)
Assignee: Institut Pasteur FR
Assignee Code: 42312

	Kind	Publication Number	Date	Application Number	Date
	B	US 6248551	20010619	US 9827900	19980223
Priority Applic:				US 9827900	19980223
Provisional Applic:				US 60-41745	19970328

Calculated Expiration: 20180223

HELICOBACTER ALIPHATIC AMIDASE **AMIE POLYPEPTIDES, AND DNA SEQUENCES ENCODING THOSE POLYPEPTIDES...**

2/3,KWIC/40 (Item 2 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

3168988 9921350
C/PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITILES; ISOLATED**

COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND AMIDASE **ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**

Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John Edward (US); Herkes Frank Edward (US)
Assignee: Du Pont de Nemours, E I & Co
Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5922589	19990713	US 98108729	19980701
Division of:		US 5858736		US 96650073	19960517
Priority Applic:				US 98108729	19980701
				US 96650073	19960517

Calculated Expiration: 20160517

PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITILES... ...ISOLATED COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND** AMIDASE **ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**

2/3,KWIC/41 (Item 3 from file: 340)
DIALOG(R)File 340:CLAIMS(R)/US Patent

3096789 9901716
C/PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITRILES; CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING** ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**
Inventors: Di Cosimo Robert (US); Fallon Robert Donald (US); Gavagan John Edward (US); Herkes Frank Edward (US)
Assignee: Du Pont de Nemours, E I & Co
Assignee Code: 25048

	Kind	Publication Number	Date	Application Number	Date
	A	US 5858736	19990112	US 96650073	19960517
Priority Applic:				US 96650073	19960517

Calculated Expiration: 20160517
CERTIFICATE OF CORRECTION: 19990928

PREPARATION OF LACTAMS FROM ALIPHATIC **ALPHA, OMEGA-DINITRILES... ...CONTACTING DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING** ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**

2/3,KWIC/43 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.

4166734
Derwent Accession: 1998-041747
Utility
C/ **Preparation of lactams from** aliphatic **[alpha],[omega]-Dinitiles** ; ISOLATED **COMAMONAS TESTOSTERONI 5-MGAM-4D WITH NITRILE HYDRATASE AND** AMIDASE **ACTIVITIES; FOR HIGH YIELD WITH HIGH REGIOSELECTIVITY AND BY PRODUCT INHIBITION**
Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE

Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5922589	A	19990713	US 98108729	19980701
Division	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 19383

Preparation of lactams from aliphatic **[alpha],[omega]-Dinitiles**

2/3,KWIC/44 (Item 3 from file: 654)
DIALOG(R)File 654:US Pat.Full.
(c) Format only 2004 The Dialog Corp. All rts. reserv.

4095232
Derwent Accession: 1998-041747
Utility
CERTIFICATE OF CORRECTION
C/ **Preparation of lactams from** aliphatic **[alpha],[omega]-dinitriles** ; CONTACTIN **G DINITRILE IN AQUEOUS MIXTURE WITH ENZYME CATALYST HAVING** ALIPHATIC **NITRILASE ACTIVITY OR COMBINATION OF NITRILE HYDRATASE AND** AMIDASE **ACTIVITY, CONTACTING PRODUCT WITH HYDROGEN AND HYDROGENATION CATALYST TO PRODUCE LACTAM**
Inventor: Di Cosimo, Robert, Rockland, DE
Fallon, Robert Donald, Elkton, MD
Gavagan, John Edward, Wilmington, DE
Herkes, Frank Edward, Wilmington, DE
Assignee: E. I. du Pont de Nemours and Company (02), Wilmington, DE
Du Pont de Nemours, E I & Co (Code: 25048)
Examiner: Lilling, Herbert J. (Art Unit: 161)

	Publication Number	Kind	Date	Application Number	Filing Date
Main Patent	US 5858736	A	19990112	US 96650073	19960517

Fulltext Word Count: 20552

Preparation of lactams from aliphatic **[alpha],[omega]-dinitriles**

2/3,KWIC/48 (Item 1 from file: 349)
DIALOG(R)File 349:PCT FULLTEXT
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00453630
i(HELICOBACTER) ALIPHATIC AMIDASE **POLYPEPTIDES, DNA SEQUENCES ENCODING THOSE POLYPEPTIDES AND USES THEREOF**
POLYPEPTIDES DE L' AMIDASE **ALIPHATIQUE AmiE D'i(HELICOBACTER)ET SEQUENCES D'ADN CODANT LESDITS POLYPEPTIDES**
Patent Applicant/Assignee:
INSTITUT PASTEUR,
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE,
DE REUSE Hilde,
SKOULOUBRIS Stephane,
LABIGNE Agnes,
Inventor(s):
DE REUSE Hilde,
SKOULOUBRIS Stephane,
LABIGNE Agnes,
Patent and Priority Information (Country, Number, Date):
Patent: WO 9844094 A2 19981008

Application: WO 98EP1824 19980327 (PCT/WO EP9801824)
Priority Application: US 9741745 19970328
Designated States: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW GH GM KE LS MW SD SZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG CI CM GA GN ML MR NE SN TD TG
Publication Language: English
Fulltext Word Count: 9017

i(HELICOBACTER) ALIPHATIC AMIDASE POLYPEPTIDES, DNA SEQUENCES ENCODING THOSE POLYPEPTIDES AND USES THEREOF
POLYPEPTIDES DE L' AMIDASE ALIPHATIQUE AmiE D'i(HELICOBACTER)ET SEQUENCES D'ADN CODANT LESDITS POLYPEPTIDES

?logoff hold
13apr04 12:19:15 User228206 Session D2146.7
$0.48 0.150 DialUnits File155
$2.31 11 Type(s) in Format 9
$2.31 11 Types
$2.79 Estimated cost File155
$0.13 0.023 DialUnits File5
$1.75 1 Type(s) in Format 9
$1.75 1 Types
$1.88 Estimated cost File5
$0.07 0.006 DialUnits File399
$0.07 Estimated cost File399
$0.12 0.006 DialUnits File440
$0.12 Estimated cost File440
$0.02 0.006 DialUnits File144
$0.02 Estimated cost File144
$0.79 0.040 DialUnits File357
$4.54 2 Type(s) in Format 3
$4.54 2 Types
$5.33 Estimated cost File357
$2.18 0.139 DialUnits File340
$4.20 3 Type(s) in Format 3
$4.20 3 Types
$6.38 Estimated cost File340
$0.68 0.115 DialUnits File654
$1.40 2 Type(s) in Format 3
$1.40 2 Types
$2.08 Estimated cost File654
$0.01 0.006 DialUnits File143
$0.01 Estimated cost File143
$0.03 0.006 DialUnits File156
$0.03 Estimated cost File156
$0.03 0.006 DialUnits File50
$0.03 Estimated cost File50
$0.09 0.023 DialUnits File65
$1.10 1 Type(s) in Format 9
$1.10 1 Types
$1.19 Estimated cost File65
$0.01 0.006 DialUnits File203
$0.01 Estimated cost File203
$0.09 0.006 DialUnits File342
$0.09 Estimated cost File342
$0.03 0.006 DialUnits File348
$0.03 Estimated cost File348
$0.16 0.035 DialUnits File349
$1.60 1 Type(s) in Format 3
$1.60 1 Types
$1.76 Estimated cost File349
OneSearch, 16 files, 0.577 DialUnits FileOS
$0.24 TELNET
$22.06 Estimated cost this search
$22.06 Estimated total session cost 0.577 DialUnits

Search Results - Record(s) 1 through 4 of 4 returned.

L7: Entry 1 of 4 File: PGPB Sep 25, 2003

PGPUB-DOCUMENT-NUMBER: 20030180330
DOCUMENT-IDENTIFIER: US 20030180330 A1

TITLE: Method for identifying helicobacter antigens
PUBLICATION-DATE: September 25, 2003

US-CL-CURRENT: 424/234.1; 435/7.32, 530/350
INT-CL: [07] G01 N 33/554, G01 N 33/569, A61 K 39/02, C07 K 14/195

L7: Entry 2 of 4 File: USPT Jun 19, 2001

US-PAT-NO: 6248551
DOCUMENT-IDENTIFIER: US 6248551 B1

TITLE: Helicobacter aliphatic amidase AmiE polypeptides, and DNA sequences encoding those polypeptides

DATE-ISSUED: June 19, 2001

US-CL-CURRENT: 435/18; 435/106, 435/228, 435/32, 435/6, 514/2, 530/344, 530/350

INT-CL: [07] A61 K 39/02

L7: Entry 3 of 4 File: DWPI Sep 25, 2003

DERWENT-ACC-NO: 2001-639461
ABSTRACTED-PUB-NO: WO 200183531A
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TITLE: Helicobacter proteins, used for producing vaccines against H. pylori infection, and related gastritis, cancers and ulcers

INT-CL (IPC): A61 K 39/02, C07 K 14/195, C07 K 14/205, G01 N 33/38, G01 N 33/554, G01 N 33/569
Derwent-CL (DC): B04, D16 , S03
CPI Codes: B04-B04C1; B14-A01; B14-E08; B14-E10B; B14-H01; B14-H01B; B14-S11B; B14-S11C; D05-H07; D05-H13;
EPI Codes: S03-E14D1; S03-E14D4; S03-E14H4;

L7: Entry 4 of 4 File: DWPI Oct 8, 1998

DERWENT-ACC-NO: 1998-557106
ABSTRACTED-PUB-NO: US 6248551B
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TITLE: New Helicobacter aliphatic amidase AmiE polypeptides and their encoding sequences - used in diagnosis, treatment and prevention of Helicobacter sp. infections in humans and animals

- INT-CL (IPC): A61 K 39/02, C12 N 9/00
  Derwent-CL (DC): B04, C06 , D16
  CPI Codes: B04-C01; C04-C01; B04-E02E; C04-E02E; B04-E08; C04-E08; B04-F0100E; C04-F0100E; B04-G21; C04-G21; B04-L05; C04-L05; B04-N03; C04-N03; B12-K04; C12-K04; B14-E08; C14-E08; D05-H12B2; D05-H14; D05-H17; D05-H17A3; D05-H19;

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